

Davis, Minh-Tam

To: Schulwitz, Paul
Subject: search for 09/700700

Thanks for your search result of SEQ ID NO:434 of 09/439313

However it seems that the search was not done against the parent cases of 09/439313, as requested, but rather against commercial data base, PGPUB and issued patents.

Could you please contact me ASAP because it is due this biweek.

Thanks.

MINH TAM DAVIS

305-2008

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STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 103561

TO: Minh-Tam Davis
Location: CM1/8A01&8E12
Art Unit: 1642
Saturday, September 13, 2003
Case Serial Number: 09/700700

From: Paul Schulwitz
Location: Biotech-Chem Library
CM1-6B06
Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

Examiner Davis,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(703)305-1954

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103561

From: Hutzell, Paula
Sent: Wednesday, September 10, 2003 1:57 PM
To: STIC-Biotech/ChemLib; Davis, Minh-Tam
Subject: FW: Rush search request for 09/700700

approved

-----Original Message-----

From: Davis, Minh-Tam
Sent: Wednesday, September 10, 2003 9:04 AM
To: Hutzell, Paula
Subject: FW: Rush search request for 09/700700

Could you approve the rush request since Christina is out of the office today?
ThanksTam

-----Original Message-----

Fr m: Davis, Minh-Tam
Sent: Wednesday, September 10, 2003 9:02 AM
To: Chan, Christina
Subject: Rush search request for 09/700700

Please search SEQ ID NO:434 in the following parent cases of 09/439313 for priority date determination.

09439313 <snquery.pl?APPL_ID=09439313>

is a continuation in part of 09352616 <snquery.pl?APPL_ID=09352616>

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Which is a continuation in part of 08904804 <snquery.pl?APPL_ID=08904804>

Which is a continuation in part of 08806099 <snquery.pl?APPL_ID=08806099>

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 9/12
Date Completed: 9/13
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 01:49:31 ; Search time 2165 Seconds
(without alignments)
9145.616 Million cell updates/sec

Title: US-09-352-616A-434

Perfect score: 484

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	484	100.0	484	6	AR261002 Sequence
2	484	100.0	484	6	AR278533 Sequence
3	484	100.0	484	6	AX106653 Sequence
4	484	100.0	484	6	AX140944 Sequence
5	484	100.0	484	6	AX200804 Sequence
6	484	100.0	484	6	AX267460 Sequence
7	472	97.5	2051	6	AR244306 Sequence
8	472	97.5	2984	6	AR237420 Sequence
9	472	97.5	2984	6	AR260913 Sequence
10	472	97.5	2984	6	AR278444 Sequence
11	472	97.5	2984	6	AX106211 Sequence
12	472	97.5	2984	6	AX106554 Sequence
13	472	97.5	2984	6	AX140845 Sequence
14	472	97.5	2984	6	AX200705 Sequence
15	472	97.5	2984	6	AX267361 Sequence
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17	471	97.3	174445	9	AC051642 Homo sapi
18	471	97.3	184361	2	AC022597 Homo sapi
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20	426.2	88.1	1020	6	AR244074 Sequence
21	426.2	88.1	1021	6	AR244075 Sequence
22	415.6	85.9	822	6	AR244195 Sequence
23	382.8	79.1	497	6	AR244194 Sequence
24	365	75.4	366	6	AR237207 Sequence
25	365	75.4	366	6	AR260700 Sequence
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ALIGNMENTS

RESULT 1
AR261002
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DEFINITION Sequence 434 from patent US 6321716.
ACCESSION AR261002
VERSION AR261002.1 GI:28071765
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 484)
AUTHORS Mashiki,Z. and Harada,J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 434 27-NOV-2001;
FEATURES Location/Qualifiers

AR261002 484 bp DNA linear PAT 29-JAN-2003

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LOCUS AX140944 484 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 434 from Patent WO0134802.
ACCESSION AX140944
VERSION AX140944.1 GI:14281041
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Retter, M.W., Stolk, J.A., Day, C.H.,
Skeiky, V.A., and Wang, A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0134802-A 434 17-MAY-2001;
CORIXA CORPORATION (US)
FEATURES
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BASE COUNT 137 a 101 c 73 g 173 t
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Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 481 TTTTA 484

RESULT 5
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DEFINITION Sequence 434 from Patent WO0151633.
ACCESSION AX200804
VERSION AX200804.1 GI:15390701
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
Stolk, J.A., Skeiky, V.A., Wang, A., and Meagher, M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 434 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
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/db_xref="taxon:9606"
BASE COUNT 137 a 101 c 73 g 173 t
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Best Local Similarity 100.0%; Pred. No. 4.5e-105;
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	481	TTTA 484	

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DEFINITION	AR244306				
ACCESSION	AR244306.1	GI:27292093			
VERSION					
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 2051)				
	Zhang, J., Astle, J.H., Carroll, E. III, Endege, W.O., Ford, D.M.,				
	Monahan, J.E., Schlegel, R. and Steinmann, K.E.				
TITLE	Genes and gene expression products that are differentially				
	regulated in prostate cancer				
JOURNAL	Patent: US 6476207-A	334 05-NOV-2002;			
FEATURES	Location/Qualifiers				
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494	CG	TGCTCAATCTCTCACA	TAAGTCTGTGACTTTGAA	GTTTAGTTCAGCAG	CCCCACCAA 435	
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Qy 479 TCCTTA 484
Db 374 TCCTTA 369

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DEFINITION Sequence 335 from patent US 6465611.
ACCESSION AR237420
VERSION AR237420.1 GI:27282078
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2984)
AUTHORS Xu,J., Dillon,D.C. and Mitcham,J.L.
TITLE Compounds for immunotherapy of prostate cancer and methods for their use
JOURNAL Patent: US 6465611-A 335 15-OCT-2002;
FEATURES Location/Qualifiers
source 1..2984
BASE COUNT 837 a 659 c 842 t 1 others
ORIGIN

Query Match 97.5%; Score 472; DB 6; Length 2984;
Best Local Similarity 99.6%; Pred. No. 2.7e-102;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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LOCUS
DEFINITION Sequence 335 from patent US 6321716.
ACCESSION AR260913
VERSION AR260913.1 GI:28071676
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2984)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate

JOURNAL Cancer
 Patent: US 6512094-A 335 28-JAN-2003;
 FEATURES Location/Qualifiers
 source 1..2984
 BASE COUNT 837 a 659 c 645 g 842 t 1 others
 ORIGIN

Query Match 97.5%; Score 472; DB 6; Length 2984;
 Best Local Similarity 99.6%; Pred. No. 2.7e-102;
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 Db 2953 TCTTTA 2958

RESULT 11
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 LOCUS 2984 bp DNA linear PAT 30-APR-2001
 DEFINITION Sequence 349 from Patent WO0125273.
 ACCESSION AX106211
 VERSION AX106211.1 GI:13921900
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Skelky, Y.A., Xu, J., Cheever, M.A. and Reed, S.G.
 Compositions and methods for wt1 specific immunotherapy
 Patent: WO 0125273-A 349 12-APR-2001;
 JOURNAL CORIXA CORPORATION (US)
 FEATURES Location/Qualifiers
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Query Match 97.5%; Score 472; DB 6; Length 2984;
 Best Local Similarity 99.6%; Pred. No. 2.7e-102;
 Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
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 QY 179 GCTTTTCCCATTTGGAAGTCTTTGTTTAAATTTACTTGGTTTGAATCCATCTT 2652
 Db 2653 GCTTTTCCCATTTGGAAGTCTTTGTTTAAATTTACTTGGTTTGAATCCATCTT 2652
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 Db 2713 AGAGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATCTGA 2712
 QY 299 GACAGCCTGTTCTATCCTCTGTTTAAATTTACTTGGTTTGAATCCATCTGA 358
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 Db 2833 CCGTCTCCATCTGTCACATAAAGTCTGTGACTTGAAGTTAGTCAGCAGCCCAAC 2832
 QY 419 ACTTTATTTCTATGTTTGAACATATGATGTTTGAATTTAGTAAAGTACCAGT 478
 Db 2893 ACTTTATTTCTATGTTTGAACATATGATGTTTGAATTTAGTAAAGTACCAGT 478
 QY 479 TCTTTA 484
 Db 2953 TCTTTA 2958

RESULT 12
 AX106554
 LOCUS 2984 bp DNA linear PAT 30-APR-2001
 DEFINITION Sequence 335 from Patent WO0125272.
 ACCESSION AX106554
 VERSION AX106554.1 GI:13922229
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Xu, J., Skelky, Y.A., Reed, S.G. and Cheever, M.A.
 Compositions and methods for therapy and diagnosis of prostate
 cancer.
 Patent: WO 0125272-A 335 12-APR-2001;
 JOURNAL CORIXA CORPORATION (US)
 FEATURES Location/Qualifiers
 source 1..2984
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 BASE COUNT 837 a 659 c 645 g 842 t 1 others
 ORIGIN

Query Match 97.5%; Score 472; DB 6; Length 2984;
 Best Local Similarity 99.6%; Pred. No. 2.7e-102;
 Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
 QY 1 TTTTAAATAAGCATTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 60
 Db 2473 TTTTAAATAAGCATTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 60

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Qy 179 GCTTTTCCCATTTGGAACCTAGTCAATTAACCCATCTCTGAACCTGGTGAAGAAACATCTGA 238
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Qy 419 ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAATAAGTACCCATG 478
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Qy 479 TCTTTA 484
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Db 2953 TCTTTA 2958

RESULT 13
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LOCUS AX140845 2984 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 335 from Patent WO0134802.
ACCESSION AX140845
VERSION AX140845.1 GI:14280952
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stoik,J.A., Day,C.H.,
Skeiky,Y.A. and Wang,A.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0134802-A 335 17-MAY-2001;
CORIXA CORPORATION (US)
FEATURES
source
Location/Qualifiers
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BASE COUNT 837 a 659 c 645 g 842 t 1 others
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Query Match 97.5%; Score 472; DB 6; Length 2984;
Best Local Similarity 99.6%; Pred. No. 2.7e-102;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 TTTTAAATAGCATTTAGTGCTCAGTCCCTACTGAGTACTCTTTCTCCCCCTCTG 60
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Qy 121 TGTTCG--AAAAAAGAGTGTCTTTGTTTAAATTTACTTGGTTGTAATCCATCTT 178
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Qy 179 GCTTTTCCCATTTGGAACCTAGTCAATTAACCCATCTCTGAACCTGGTGAAGAAACATCTGA 238
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Qy 299 GACAGCTGTTTCTATCCTGTTTAATAAATAGTTGGTTCTCAGAACCATTTTCAACCA 358
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Qy 479 TCTTTA 484
|||||
Db 2953 TCTTTA 2958

RESULT 14
AX200705
LOCUS AX200705 2984 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 335 from Patent WO0151633.
ACCESSION AX200705
VERSION AX200705.1 GI:15390594
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 335 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source
Location/Qualifiers
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/mol_type="genomic DNA"
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BASE COUNT 837 a 659 c 645 g 842 t 1 others
ORIGIN
Query Match 97.5%; Score 472; DB 6; Length 2984;
Best Local Similarity 99.6%; Pred. No. 2.7e-102;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 TTTTAAATAGCATTTAGTGCTCAGTCCCTACTGAGTACTCTTTCTCCCCCTCTG 60
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Qy 179 GCTTTTCCCATTTGGAACCTAGTCAATTAACCCATCTCTGAACCTGGTGAAGAAACATCTGA 238
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GenCore version 5.1.6		Copyright (c) 1993 - 2003 CompuGen Ltd.	
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5	484	100.0 484 22	AAH02834 Prostate tumour an
6	484	100.0 484 24	ABL95233 Human 22595 cDNA s
7	484	100.0 484 25	ACA59670 Prostate cancer th
8	473	97.7 755 21	AAFI5823 Human prostate can

c	9	472	97.5	2051	21	AAZ97473	Human prostate can
	10	472	97.5	2984	21	AAA06564	Human immunogenic
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	15	472	97.5	2984	22	AAAF86953	Human p705P invent
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	17	472	97.5	2984	25	ACA59581	Prostate cancer th
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	20	448	92.6	1191	23	ABV24721	Human prostate exp
	21	448	92.6	1191	23	ABV24938	Human prostate can
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	23	426.2	88.1	1021	21	AAZ97242	Human prostate can
	24	415.6	85.9	822	21	AAZ97362	Human prostate can
	25	382.8	79.1	497	21	AAZ97361	Human prostate can
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	31	365	75.4	366	22	AAH93467	Human prostate-spe
	32	365	75.4	366	22	AAH84781	Human prostate-spe
	33	365	75.4	366	22	AAH02532	Prostate tumour an
	34	365	75.4	366	24	ABS71256	Human prostate tum
	35	365	75.4	366	24	ABS58640	Prostate tumour CD
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ALIGNMENTS	
RESULT 1	
AAA06653	
ID	AAA06653 standard; cDNA; 484 BP.
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AC	AAA06653;
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DT	13-JUN-2000 (first entry)
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DE	Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:434.
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KW	Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW	immunogenic; cytostatic; vaccine; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200004149-A2.
XX	
PD	27-JAN-2000.
XX	
PF	14-JUL-1999; 99WO-US15838.
XX	
PR	14-JUL-1998; 98US-0115453.
PR	14-JUL-1998; 98US-0116134.
PR	23-SEP-1998; 98US-0159812.
PR	23-SEP-1998; 98US-0159822.
PR	15-JAN-1999; 99US-0232149.
PR	15-JAN-1999; 99US-0232880.
PR	09-APR-1999; 99US-0288946.
XX	
PA	(CORI-) CORIXA CORP.
XX	

PI Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;
XX WPI; 2000-171268/15.
DR
XX
XX
PT New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein -
XX
XX
PS Claim 1; Page 250; 263pp; English.
XX
CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumor protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AA06241 to AA06691 and
CC AY82000 to AY82020 represent sequences used in the exemplification of
CC the present invention.
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SQ Sequence 484 BP; 137 A; 101 C; 73 G; 173 T; 0 other;
Query Match 100.0%; Score 484; DB 21; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.4e-116; Indels 0; Gaps 0;
Matches 484; Conservative 0; Mismatches 0;
QY 1 TTTTAAATAAGCAATTTAGTCTAGTCCCTACTGAGTACTCTTTCTCTCCCTCTCTG 60
DB 1 TTTTAAATAAGCAATTTAGTCTAGTCCCTACTGAGTACTCTTTCTCTCCCTCTCTG 60
QY 61 AATTTAATCTTTCAACTTGCATTTGCAAGGATTACACATTTCACTGATGATATATG 120
DB 61 AATTTAATCTTTCAACTTGCATTTGCAAGGATTACACATTTCACTGATGATATATG 120
QY 121 TTTTCAAAAAAAGTCTTTCTTTAAATTAATTTAGTGGTTGTGATCATCTTGC 180
DB 121 TTTTCAAAAAAAGTCTTTCTTTAAATTAATTTAGTGGTTGTGATCATCTTGC 180
QY 181 TTTTCCCAATGGAATAGTCAATTAACCCATCTCTGAGTGGTAGAAAAACATCTGAAG 240
DB 181 TTTTCCCAATGGAATAGTCAATTAACCCATCTCTGAGTGGTAGAAAAACATCTGAAG 240
QY 241 AGCTAGTCTATGAGTCTGACAGTGGAATTTGATGATGTTCTCAGAACCATTTTCAACCCAGA 300
DB 241 AGCTAGTCTATGAGTCTGACAGTGGAATTTGATGATGTTCTCAGAACCATTTTCAACCCAGA 300
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DB 481 TTTA 484
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ID AAS63862 standard; cDNA; 484 BP.
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AC AAS63862;
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DT 29-JAN-2002 (first entry)

XX Human prostate cDNA sequence #398.
DE
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XX
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
DR WPI; 2001-639232/73.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
the diagnosis and treatment of cancer, especially prostate cancer -
PS Claim 1; Page 375; 579pp; English.
XX
XX The invention relates to isolated prostate-specific
polynucleotides, polypeptides, fusion proteins of the polypeptides,
antibodies raised against the polypeptides (or antigenic epitopes,
derived from them) and antigen-presenting cells expressing the
polypeptides. The antibodies are useful for detecting the presence of
cancer, especially prostate cancer. The polypeptides, polynucleotides and
the antigen-presenting cells are useful for stimulating the presence of
t cells specific for a tumour protein, and for inhibiting the development
of cancer especially prostate cancer. Compositions comprising an immune
polynucleotide and/or polypeptide are useful for stimulating an immune
response, and for treating cancer. The oligonucleotide is useful for
detecting cancer. The present sequence is a prostate specific
polynucleotide of the invention.
XX
SQ Sequence 484 BP; 137 A; 101 C; 73 G; 173 T; 0 other;
Query Match 100.0%; Score 484; DB 22; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.4e-116;
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTAAATAAGCAATTTAGTCTAGTCCCTACTGAGTACTCTTTCTCTCCCTCTCTG 60
DB 1 TTTTAAATAAGCAATTTAGTCTAGTCCCTACTGAGTACTCTTTCTCTCCCTCTCTG 60
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DB 61 AATTTAATCTTTCAACTTGCATTTGCAAGGATTACACATTTCACTGATGATATATG 120
QY 121 TGTGTCAAAAAAAGTCTTTGTTTAAATTAATTTAGTGGTTGTGAAATTCATCTTGC 180
DB 121 TGTGTCAAAAAAAGTCTTTGTTTAAATTAATTTAGTGGTTGTGAAATTCATCTTGC 180
QY 181 TTTTCCCAATGGAATAGTCAATTAACCCATCTCTGAGTGGTAGAAAAACATCTGAAG 240
DB 181 TTTTCCCAATGGAATAGTCAATTAACCCATCTCTGAGTGGTAGAAAAACATCTGAAG 240

RESULTS

RESUL 4
AAH85083
ID AAH85083
XX
AC AAH85083;

DT 25-SEP-2001 (first entry)

Human prostate-specific cDNA sequence 22595-

Human; prostate cancer; therapy; diagnosis; cat eye syndrome; chromosome 22q11.2; prostate-specific protein; chromosome 1; prostate specific antigen; PSA; ss.

XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
XX

DR WPI; 2001-308785/32.
 XX Isolated polypeptide comprising at least an immunogenic portion of a
 PT prostate-specific protein, useful in the diagnosis and therapy of a
 PT prostate cancer -
 XX
 PS
 PS Claim 5; Page 273; 325pp; English.
 XX
 XX The present invention describes an isolated polypeptide (P1) comprising
 CC at least an immunogenic portion of a prostate-specific protein, or its
 CC variant. Also described are polynucleotides (N1) encoding (P1), or its
 CC (N1) have cytostatic activity and can be used in vaccine production.
 CC The polypeptides, nucleic acids and antibodies from the present
 CC invention are useful in the diagnosis and therapy of prostate cancer.
 CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
 CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
 CC region. Prostate specific antigen (PSA) P501S was located on
 CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
 CC polynucleotide and polypeptide sequences used in the exemplification
 CC of the present invention.
 XX
 XX Sequence 484 BP; 137 A; 101 C; 73 G; 173 T; 0 other;

Query Match 100.0%; Score 484; DB 22; Length 484;
 Best Local Similarity 100.0%; Pred. No. 1.4e-116;
 Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTTCTTCTCCCTCTCTG 60
 Db 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTTCTTCTCCCTCTCTG 60
 QY 61 AATTTAAATCTTCACTTGAATTTGCAAGGATTACACATTTTCACTGTGATGATATG 120
 Db 61 AATTTAAATCTTCACTTGAATTTGCAAGGATTACACATTTTCACTGTGATGATATG 120
 QY 121 TGTTCGAAAAAATAAGTCTCTTGTGTTAAATTAATTAATTAATTAATTAATTAATTA 180
 Db 121 TGTTCGAAAAAATAAGTCTCTTGTGTTAAATTAATTAATTAATTAATTAATTAATTA 180
 QY 181 TTTTTCCTCCATTTGAACTAGTCTTAACTTGAATTTGCAAGGATTACACATTTTCACTGTG 240
 Db 181 TTTTTCCTCCATTTGAACTAGTCTTAACTTGAATTTGCAAGGATTACACATTTTCACTGTG 240
 QY 241 AGCTAGTCTATCAGCATCTGACAGGTTGATTTGATTTGATTTGATTTGATTTGATTTG 300
 Db 241 AGCTAGTCTATCAGCATCTGACAGGTTGATTTGATTTGATTTGATTTGATTTGATTTG 300
 QY 301 CAGCCTGTTTCTATCTCTGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
 Db 301 CAGCCTGTTTCTATCTCTGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
 QY 361 TGCTCCAACTGTCACATAAAAGTCTGTGACTTTGATTTGATTTGATTTGATTTGATTTG 420
 Db 361 TGCTCCAACTGTCACATAAAAGTCTGTGACTTTGATTTGATTTGATTTGATTTGATTTG 420
 QY 421 TTTATTTTCTATGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 480
 Db 421 TTTATTTTCTATGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 480
 QY 481 TTTA 484
 Db 481 TTTA 484

RESULT 5
 AAH02834
 ID AAH02834 standard; cDNA; 484 BP.
 XX
 AC AAH02834;
 XX
 DT 14-JUN-2001 (first entry)
 XX
 DE Prostate tumour antigen cDNA sequence for 22595.

XX Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
 KW prostate cancer; immunogenic; cytostatic; vaccine; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200125272-A2.
 XX
 PD 12-APR-2001.
 XX
 PF 04-OCT-2000; 2000WO-US27464.
 XX
 PR 04-OCT-1999; 99US-0157455.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Skeiky YAW, Reed SG, Cheever MA;
 XX WPI; 2001-245062/25.
 DR
 XX Prostate specific protein and its encoding polynucleotide, useful for
 PT the treatment and diagnosis of prostate cancer -
 PT
 PS Claim 4; Page 256; 276pp; English.
 XX
 CC The present invention describes an isolated polypeptide (I) comprising
 CC at least an immunogenic portion of a prostate tumour antigen protein or
 CC its variant. (I) have cytostatic activity and can be used in vaccine
 CC production. (I), prostate tumour antigen polynucleotides, an antigen
 CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
 CC pharmaceutical composition containing (I) are useful for inhibiting the
 CC development of cancer in a patient. Antibodies specific for prostate
 CC specific proteins and oligonucleotides that hybridize to a
 CC polynucleotide that encodes a prostate specific protein are useful
 CC for detecting the presence or absence of a cancer or monitoring the
 CC progression the progression of a cancer, especially prostate cancer.
 CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 484 BP; 137 A; 101 C; 73 G; 173 T; 0 other;

Query Match 100.0%; Score 484; DB 22; Length 484;
 Best Local Similarity 100.0%; Pred. No. 1.4e-116;
 Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTTCTTCTCCCTCTCTG 60
 Db 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTTCTTCTCCCTCTCTG 60
 QY 61 AATTTAAATCTTCACTTGAATTTGCAAGGATTACACATTTTCACTGTGATGATATG 120
 Db 61 AATTTAAATCTTCACTTGAATTTGCAAGGATTACACATTTTCACTGTGATGATATG 120
 QY 121 TGTTCGAAAAAATAAGTCTCTTGTGTTAAATTAATTAATTAATTAATTAATTAATTA 180
 Db 121 TGTTCGAAAAAATAAGTCTCTTGTGTTAAATTAATTAATTAATTAATTAATTAATTA 180
 QY 181 TTTTTCCTCCATTTGAACTAGTCTTAACTTGAATTTGCAAGGATTACACATTTTCACTGTG 240
 Db 181 TTTTTCCTCCATTTGAACTAGTCTTAACTTGAATTTGCAAGGATTACACATTTTCACTGTG 240
 QY 241 AGCTAGTCTATCAGCATCTGACAGGTTGATTTGATTTGATTTGATTTGATTTGATTTG 300
 Db 241 AGCTAGTCTATCAGCATCTGACAGGTTGATTTGATTTGATTTGATTTGATTTGATTTG 300
 QY 301 CAGCCTGTTTCTATCTCTGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
 Db 301 CAGCCTGTTTCTATCTCTGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
 QY 361 TGCTCCAACTGTCACATAAAAGTCTGTGACTTTGATTTGATTTGATTTGATTTGATTTG 420
 Db 361 TGCTCCAACTGTCACATAAAAGTCTGTGACTTTGATTTGATTTGATTTGATTTGATTTG 420

Qy	421	TTTTATTTCTATGCTGTTTTTGGCAACATATGAGTGTGTTTGAAGAAATAAAGTACCCATGTC	480
Db	421	TTTTATTTCTATGCTGTTTTTGGCAACATATGAGTGTGTTTGAAGAAATAAAGTACCCATGTC	480
Qy	481	TTTA 484	
Db	481	TTTA 484	

RESULT 6

ABL95233

ID ABL95233 standard; cDNA: 484 BP.

XX

AC ABL95233;

XX

DT	19-JUL-2002 (first entry)
XX	Human 22595 cDNA sequence SEQ ID NO 434.
DE	
XX	
KW	Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; gene therapy; gene; ss.
KW	

LI SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
WPI; 2002-255649/30.
New prostate-specific polynucleotides for diagnosing and treating
diseases, in particular prostate cancer, and as markers for the
progression of cancer -
Claim 1; SEQ ID NO 434; 87pp; English.
The present invention provides prostate-specific coding sequences and
their encoded proteins. These can be used in the diagnosis and treatment
of cancers, particularly prostate cancer. The present sequence is a CDNA
described in the invention.
Sequence 484 BP: 137 A; 101 C; 73 G; 173 T; 0 other;

RESULTS

ACA59670

ACA59670
ID ACA59670 standard: cDNA: 484 BP.

XX
XX

ACA59670;

XX

DT 10-JUN-2003 (first entry)
XX Prostate cancer therapy associated cDNA #413.
DE
XX
XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;
KW Prostatic acid phosphatase; PAP; prostate specific membrane antigen
KW pSMA; gene; ss.

OS Homo sapiens.
XX US2002192763-A1.
PN 19-DEC-2002.
PD 29-JUN-2001; 2001US-0895793.
XX 17-APR-2000; 2000US-157455P.
PR 04-OCT-2000; 2000US-0679272.
PR 28-MAR-2001; 2001US-0822827.
XX (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEL/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW Hepler WT, Henderson RA, Hural J;
PI McNeill PD, Houghton RL, Y De Bassols CV, Foy TM;
XX WPI; 2003-352711/33.
DR
XX
PT New fusion protein comprising prostate-specific polypeptides, or its
PT immunogenic portions, useful for diagnosing, preventing and/or treating
PT cancer, particularly prostate cancer
XX
PS Example 14; SEQ ID NO 434; 85pp; English.
XX
CC The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 35 sequences defined in the USPTO
CC web site, which is encoded by any of the 4 nucleotide sequences not
CC defined in the specification. The fusion protein, composition and
CC methods are useful for diagnosing, preventing and/or treating cancer,
CC particularly prostate cancer. The proteins are useful as markers to
CC indicate the presence or absence of cancer. This sequence
CC represents a prostate cancer therapy associated cDNA.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from the US patent office at
CC seqdata.uspto.gov/sequence.html?docID=US20020192763.
XX
SQ Sequence 484 BP; 137 A; 101 C; 73 G; 173 T; 0 other;
Query Match
Best Local Similarity 100.0%; Score 484; DB 25; Length 484;
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTAAATAAGCATTTAGTCTCAGTCTCCTACTGAGTACTCTTCTCTCCCTCCCTCTG 60
DB 1 TTTTAAATAAGCATTTAGTCTCAGTCTCCTACTGAGTACTCTTCTCTCCCTCCCTCTG 60

QY 61 AATTAAATCTTTCAACTTGGCAATTTGCAAGGATTACACATTTCACTGTGATGATATG 120
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 120
QY 61 AATTAAATCTTTCAACTTGGCAATTTGCAAGGATTACACATTTCACTGTGATGATATG 120
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 120
QY 121 TGTGCAAAAAAAGAGTGTCTTTGTTTAAATTAATTTACTTGTGTTGTGAATCCATCTTGC 180
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 180
QY 121 TGTGCAAAAAAAGAGTGTCTTTGTTTAAATTAATTTACTTGTGTTGTGAATCCATCTTGC 180
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 180
QY 181 TTTTCCCATTTGGAACTAGTCAATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAG 240
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 240
QY 181 TTTTCCCATTTGGAACTAGTCAATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAG 240
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 240
QY 241 AGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGTTCTCAGAACATTTTCCACCAGA 300
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 300
QY 241 AGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGTTCTCAGAACATTTTCCACCAGA 300
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 300
QY 301 CAGCCTGTTCTATCCTCTTTTAAATAATTTAGTTTGGGTTCTCTACATGATATAAACC 360
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 360
QY 301 CAGCCTGTTCTATCCTCTTTTAAATAATTTAGTTTGGGTTCTCTACATGATATAAACC 360
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 360
QY 361 TGCTCCAATCTGTACATAAAAGTCTGACTTTGAAGTTTGTAGTCAGACCCCCCACCAC 420
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 420
QY 361 TGCTCCAATCTGTACATAAAAGTCTGACTTTGAAGTTTGTAGTCAGACCCCCCACCAC 420
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 420
QY 421 TTTATTTTCTATGTTGTTTTCACACATATGATGTTTGAATAAATAAGTACCCATGTC 480
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 480
QY 421 TTTATTTTCTATGTTGTTTTCACACATATGATGTTTGAATAAATAAGTACCCATGTC 480
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 480
QY 481 TTTA 484
DB |||||
QY 481 TTTA 484
DB |||||
RESULT 8
AAF15823
ID AAF15823 standard; cDNA; 755 BP.
XX
AC AAF15823;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:258.
XX
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnary; gastrointestinal; nephrotropic; antineoplastic; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease; ss.
XX
OS Homo sapiens.
XX
PN WO200055174-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05988.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587513/55.
DR P-PSDB; AAB56620.
XX
PT Prostate cancer associated gene sequences, referred to as prostate
PT cancer antigens, useful for treatment, prevention, and diagnosis of
PT disorders such as prostate cancer
XX
PS Claim 1; Page 781; 2338pp; English.

XX
CC AAF1566 to AAF1605 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC The prostate cancer antigens can have neuroprotective, cytostatic,
CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention.

Sequence 755 BP; 217 A; 161 C; 128 G; 246 T; 3 other;

Query Match	97.78;	Score 473;	DB 21;	Length 755;
Best Local Similarity	99.8%;	Pred. No. 1.2e-113;		
Matches 484;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;
QY	1	TTTTAAATAAGCATTTAGTGCAGTCCCTACTAGTACTCTTTCTCTCCCTCCCTCG	60	
DB	242	TTTTAAATAAGCATTTAGTGCAGTCCCTACTAGTACTCTTTCTCTCCCTCCCTCG	301	
QY	61	AATTTAATCTTTCAACTTCGCAATTTGCAAGGATTACACATTTTCACGTGTGATGTATATTG	120	
DB	302	AATTTAATCTTTCAACTTCGCAATTTGCAAGGATTACACATTTTCACGTGTGATGTATATTG	361	
QY	121	TGTTGC-AAAAAATAAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCATCTTG	179	
DB	362	TGTTGCAAAAAATAAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCATCTTG	421	
QY	180	CTTTTTCGCCATGGGAAGTACTGATTAATCAATCAATCTCTGAACTGCTGAGAAACATCTGAA	239	
DB	422	CTTTTTCGCCATGGGAAGTACTGATTAATCAATCAATCTCTGAACTGCTGAGAAACATCTGAA	481	
QY	240	GAGCTAGTCTPATCAGCATCTGACAGGTGAAATTTGGATGGTCTCAGAACCATTTTCACCCAG	299	
DB	482	GAGCTAGTCTPATCAGCATCTGACAGGTGAAATTTGGATGGTCTCAGAACCATTTTCACCCAG	541	
QY	300	ACAGCCTGTTCTATCTCTGTTTAAATAATTTAGTTTGGTGTCTCTACATGATCAATAACAAC	359	
DB	542	ACAGCCTGTTCTATCTCTGTTTAAATAATTTAGTTTGGTGTCTCTACATGATCAATAACAAC	601	
QY	360	CTGCTCCAATCTGTGCATATAAAGTCTGTGACTTGAAGTTTAGTCAGACCCCCACCAAAA	419	
DB	602	CTGCTCCAATCTGTGCATATAAAGTCTGTGACTTGAAGTTTAGTCAGACCCCCACCAAAA	661	
QY	420	CTTTATTTTCTATGTGTTTGTGCAACATATAGTGTGTTTGAATAATAAGTACCCATGT	479	
DB	662	CTTTATTTTCTATGTGTTTGTGCAACATATAGTGTGTTTGAATAATAAGTACCCATGT	721	
QY	480	CTTTA 484		
DB	722	CTTTA 726		

RESULT 9	
AAZ97473/c	
ID	AAZ97473 standard; cDNA; 2051 BP.
XX	
XX	
AC	AAZ97473;
AC	
XX	
XX	
DT	18-APR-2000 (first entry)
XX	
XX	
DE	Human prostate cancer differentially expressed gene #334.
XX	
XX	
KW	Prostate cancer specific gene; cancer; tumour progression; diagnosis;
KW	hyperproliferative cell growth; prostatic disorder; treatment;
KW	metastatic prostate cancer; benign prostate hyperplasia; BPH; ss.
XX	
XX	

OS	Homo sapiens.
XX	WO9964594-A2.
XX	16-DEC-1999.
XX	10-JUN-1999; 99WO-USL3181.
XX	11-JUN-1998; 98US-0088877.
PR	09-JUN-1999; 99US-0088877.
XX	(CHIR) CHIRON CORP.
XX	Astel JH, Carroll E, Endege WO, Ford DM, Monahan JE, Schlegel R;
PI	Steinmann KE, Zhang J;
DR	WPI; 2000-116541/10.
XX	New isolated prostate cancer specific nucleic acids, used to develop
PT	products for the diagnosis and treatment of cancer -
XX	Claim 2; Page 209-210; 212pp; English.
XX	This sequence represents a prostate cancer specific nucleic acid
CC	sequence. The invention relates to a method for diagnosing cancer,
CC	tumour progression, hyperproliferative cell growth or accompanying
CC	biological and physical manifestations. The method involves contacting
CC	the biological sample with a probe that comprises a sequence capable of
CC	hybridising to any of the 339 nucleotide sequences given in the
CC	specification (see AA97140-297478) and detecting duplex formation. The
CC	products and methods of the invention can be used for the diagnosis,
CC	prognosis, and treatment of cancer, tumour progression,
CC	hyperproliferative cell growth, and accompanying physical and biological
CC	manifestations. They can be used particularly for prostatic disorders
CC	such as metastatic prostate cancer, localised prostate cancer, or benign
CC	prostate hyperplasia (BPH).
XX	
SQ	Sequence 2051 BP: 630 A; 427 C; 408 G; 555 T; 31 other;
	Query Match 97.5%; Score 472; DB 21; Length 2051;
	Best Local Similarity 99.6%; Pred. No. 2.9e-113;
	Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
Qy	1 TTTTAAATAAGCATTTAGTGCTCAGTCCCTACTGACTACTCTTCTCCCCCTCCTCG 60
Dd	
	854 TTTTAAATAAGCATTTAGTGCTCAGTCCCTACTGACTACTCTTCTCCCCCTCCTCG 795
Qy	61 AATTTAATTCTTCAACTTCGAATTTGCCAGGATTACACATTTCACTGTGATGTATATTG 120
Dd	
	794 AATTTAATTCTTCAACTTCGAATTTGCCAGGATTACACATTTCACTGTGATGTATATTG 735
Qy	121 TGTTGC--AAAAAAAAGTGTCCTTTGTTTTAAATTAATCTGGTTTGTCAAATCCATCTT 178
Dd	
	734 TGTTGCAAAAAAAAAAGTGTCCTTTGTTTTAAATTAATCTGGTTTGTGAATCCATCTT 675
Qy	179 GCTTTTCCCATTGGAACTAGTCATTAAACCCTCTCTGAACCTGGTAGAAAAACATCTGA 238
Dd	
	674 GCITTTTCCCATTGGAAC TAGTCATTAAACCCTCTCTGAACCTGGTAGAAAAACATCTGA 615
Qy	239 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTTCTCAGAACCATTTACCCCA 298
Dd	
	614 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTTCTCAGAACCATTTACCCCA 555
Qy	299 GACAGCTGTTTCTATACCTGTTTAAATAAATAGTTTGGGTTCTCTACATGCATAACAAC 358
Dd	
	554 GACAGCTGTTTCTATACCTGTTTAAATAAATAGTTTGGGTTCTCTACATGCATAACAAC 495
Qy	359 CCTGCTCCAATCTGTACATAAAAGTCTGTGACTTTGAAGTTTGTAGTCAGCACCCACCAA 418
Dd	
	494 CCTGCTCCAATCTGTACATAAAGTCTGTGACTTTGAAGTTTGTAGTCAGCACCCACCAA 435
Qy	419 ACTTTATTTTCTATGTGTTTTTTTGGCAACATATGAGTGTTTTGGAAATTAAGTACCCATG 478
Dd	

Db 434 ACTTTATTTTCTATGTGTTTTTTGCAACATATGAGTCTTTTGAATAAGTACCATG 375

Qy 479 TCTTTA 484
|||||

Db 374 TCTTTA 369

RESULT 10
AAA06564
ID AAA06564 standard; cDNA; 2984 BP.
XX AC
XX AAA06564;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:335.
XX Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
XX WO200004149-A2.
XX
XX 27-JAN-2000.
XX
XX 14-JUL-1999; 99WO-US15838.
XX
XX 14-JUL-1998; 98US-0115453.
XX PR 14-JUL-1998; 98US-0116134.
XX PR 23-SEP-1998; 98US-0159812.
XX PR 23-SEP-1998; 98US-0159822.
XX PR 15-JAN-1999; 99US-0232149.
XX PR 15-JAN-1999; 99US-0232880.
XX PR 09-APR-1999; 99US-0288946.
XX
XX (CORI-) CORIXA CORP.
XX
XX Dillon DC, Harlocker SL, Yuglu J, Xu J, Mitcham JL;
XX WPI; 2000-171268/15.
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
XX comprises an immunogenic portion of prostate tumor protein -
XX
XX Claim 50; Page 207-208; 263pp; English.
XX
XX The present invention describes isolated polypeptides, comprising an
XX immunogenic portion of a prostate tumour protein (PTP). The polypeptides
XX and polynucleotides encoding them have cytostatic activity and can be
XX used in vaccines and in gene therapy. The polypeptides and
XX polynucleotides encoding them, antigen presenting cells which express
XX the polypeptides, antibodies against the polypeptides and vaccines
XX comprising them can be used for inhibiting the development of prostate
XX cancer in a patient. The polypeptides can be used to generate antibodies
XX or anti-idiotypic antibodies for passive immuno therapy. A portion of
XX the polynucleotides encoding the polypeptides can be used as a probe or
XX to modulate the expression of the polypeptides. AAA06241 to AAA06691 and
XX AA82000 to AA82030 represent sequences used in the exemplification of
XX the present invention.
XX
SQ Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;
Query Match 97.5%; Score 472; DB 21; Length 2984;
Best Local Similarity 99.6%; Pred. No. 3,2e-113;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
Qy 1 TTTTAAATAAGCATTTAGTGTCTAGTCCCTACTGAGTACTCTTTCTCTCCCTCTCTG 60
Db 2473 TTTTAAATAAGCATTTAGTGTCTAGTCCCTACTGAGTACTCTTTCTCTCCCTCTCTG 2532
Qy 61 AATTAAATCTTTCAACTTGAATTTGAAGSATTACACATTTCACGTGTGATTAATG 120
|||||

```
XX PS Claim 1; Page 335-336; 579pp; English.
XX CC The invention relates to isolated prostate-specific
XX CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
XX CC antibodies raised against the polypeptides (or antigenic epitopes
XX CC derived from them) and antigen-presenting cells expressing the
XX CC polypeptides. The antibodies are useful for detecting the presence of
XX CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
XX CC the antigen-presenting cells are useful for stimulating and/or expanding
XX CC T cells specific for a tumour protein, and for inhibiting the development
XX CC of cancer especially prostate cancer. Compositions comprising the
XX CC polynucleotide and/or polypeptide are useful for stimulating an immune
XX CC response, and for treating cancer. The oligonucleotide is useful for
XX CC detecting cancer. The present sequence is a prostate specific
XX CC polynucleotide of the invention.
XX SQ Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;

Query Match          97.5%; Score 472; DB 22; Length 2984;
Best Local Similarity 99.6%; Pred. No. 3.2e-113;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 TTTTAAATAAGCAATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 60
Db 2473 TTTTAAATAAGCAATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 2532
Qy 61 AATTTAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATG 120
Db 2533 AATTTAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATG 2592
Qy 121 TGTGTC--AAAAAAGTGTCTTTGTTTAAATTTACTTGGTTGTGAATCCATCTT 178
Db 2593 TGTGTC--AAAAAAGTGTCTTTGTTTAAATTTACTTGGTTGTGAATCCATCTT 2652
Qy 179 GCTTTTCCCAATTTGGAAGTGTCTTAAACCCATCTCTGAACTGTGAATTAACATCTGA 238
Db 2653 GCTTTTCCCAATTTGGAAGTGTCTTAAACCCATCTCTGAACTGTGAATTAACATCTGA 2712
Qy 239 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTTCTCAGAACCAATTCACCCA 298
Db 2713 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTTCTCAGAACCAATTCACCCA 2772
Qy 299 GACAGCCTGTTTCTATCCTGTTTAAATTTAGTTTGGGTTCTCTACATGATGATGAACAA 358
Db 2773 GACAGCCTGTTTCTATCCTGTTTAAATTTAGTTTGGGTTCTCTACATGATGATGAACAA 2832
Qy 359 CCTGCTCCATCTGTACATATAAAGTCTGTGACTTGAAGTTTAGTCAGCACCCCAACCA 418
Db 2833 CCTGCTCCATCTGTACATATAAAGTCTGTGACTTGAAGTTTAGTCAGCACCCCAACCA 2892
Qy 419 ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTCTTTGAAATATAAAGTACCCATG 478
Db 2893 ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTCTTTGAAATATAAAGTACCCATG 2952
Qy 479 TCTTTA 484
Db 2953 TCTTTA 2958

RESULT 12
AAH93680
ID AAH93680 standard; cDNA; 2984 BP.
XX AC AAH93680;
XX AC AAH93680;
XX DF 04-OCT-2001 (first entry)
XX DE Human prostate-specific cDNA sequence p705P.
XX DE Human; prostate cancer; prostate-specific; diagnosis; vaccine;
XX KW cytostatic; gene therapy; metastasis; ss.
XX
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OS Homo sapiens.
XX PN WO200151633-A2.
XX PD 19-JUL-2001.
XX PF 16-JAN-2001; 2001WO-US01574.
XX PR 14-JAN-2000; 2000US-0483672.
XX PA (CORI-) CORIXA CORP.
XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAW;
PI Wang A, Meagher MJ;
XX DR WPI; 2001-425873/45.
XX PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX PS Claim 1; Page 333-334; 543pp; English.
XX CC The present invention describes polynucleotide sequences (I) which encode
XX CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
XX CC and can be used in vaccine production and gene therapy. (I), (II),
XX CC antibodies to (II), fusion proteins comprising (II), and isolated
XX CC T cells prepared using (I) or (II) are used in the detection of cancer in a
XX CC patient. The cancer that is diagnosed or treated is particularly
XX CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
XX CC (I) and (II) can also be used to improve diagnostic and therapeutic
XX CC methods for prostate cancer. They can indicate the level of metastasis
XX CC as well as the prostate volume. AAH93357 to AAH93944 and AAH0115 to
XX CC AAH01318 represent polynucleotide and amino acid sequences used in the
XX CC exemplification of the present invention.
XX SQ Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;

Query Match          97.5%; Score 472; DB 22; Length 2984;
Best Local Similarity 99.6%; Pred. No. 3.2e-113;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 TTTTAAATAAGCAATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 60
Db 2473 TTTTAAATAAGCAATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 2532
Qy 61 AATTTAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATG 120
Db 2533 AATTTAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATG 2592
Qy 121 TGTGTC--AAAAAAGTGTCTTTGTTTAAATTTACTTGGTTGTGAATCCATCTT 178
Db 2593 TGTGTC--AAAAAAGTGTCTTTGTTTAAATTTACTTGGTTGTGAATCCATCTT 2652
Qy 179 GCTTTTCCCAATTTGGAAGTGTCTTAAACCCATCTCTGAACTGTGAATTAACATCTGA 238
Db 2653 GCTTTTCCCAATTTGGAAGTGTCTTAAACCCATCTCTGAACTGTGAATTAACATCTGA 2712
Qy 239 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTTCTCAGAACCAATTCACCCA 298
Db 2713 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTTCTCAGAACCAATTCACCCA 2772
Qy 299 GACAGCCTGTTTCTATCCTGTTTAAATTTAGTTTGGGTTCTCTACATGATGATGAACAA 358
Db 2773 GACAGCCTGTTTCTATCCTGTTTAAATTTAGTTTGGGTTCTCTACATGATGATGAACAA 2832
Qy 359 CCTGCTCCATCTGTACATATAAAGTCTGTGACTTGAAGTTTAGTCAGCACCCCAACCA 418
Db 2833 CCTGCTCCATCTGTACATATAAAGTCTGTGACTTGAAGTTTAGTCAGCACCCCAACCA 2892
Qy 419 ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTCTTTGAAATATAAAGTACCCATG 478
Db 2893 ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTCTTTGAAATATAAAGTACCCATG 2952
Qy 479 TCTTTA 484
Db 2953 TCTTTA 2958

RESULT 12
AAH93680
ID AAH93680 standard; cDNA; 2984 BP.
XX AC AAH93680;
XX AC AAH93680;
XX DF 04-OCT-2001 (first entry)
XX DE Human prostate-specific cDNA sequence p705P.
XX DE Human; prostate cancer; prostate-specific; diagnosis; vaccine;
XX KW cytostatic; gene therapy; metastasis; ss.
XX
```

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QY 419 ACTTATATTTCTGATGCTGTTTTTTCACACATATGAGTCTTTTGAATAAAGTACCCATG 478
Db 2893 ACTTATATTTCTGATGCTGTTTTTTCACACATATGAGTCTTTTGAATAAAGTACCCATG 2952
QY 479 TCTTTTA 484
Db 2953 TCTTTTA 2958

RESULT 13
AAH84994
ID AAH84994 standard; cDNA; 2984 BP.
AC AAH84994;
XX
XX
XX 25-SEP-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence P705P/9-F3.
KW Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA; ss.
XX
OS Homo sapiens.
XX
XX WO200134802-A2.
XX
XX PD 17-MAY-2001.
XX
XX PF 09-NOV-2000; 2000WO-US30904.
XX
XX PR 12-NOV-1999; 99US-0439313.
XX PR 18-NOV-1999; 99US-0443686.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
XX PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
XX
XX DR WPI; 2001-308785/32.
XX
XX PT Isolated polypeptide comprising at least an immunogenic portion of a
XX PT prostate-specific protein, useful in the diagnosis and therapy of
XX PT prostate cancer -
XX
XX PS Claim 31; Page 233-234; 325pp; English.
XX
XX CC The present invention describes an isolated polypeptide (P1) comprising
XX CC at least an immunogenic portion of a prostate-specific protein, or its
XX CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
XX CC (N1) have cytostatic activity and can be used in vaccine production.
XX CC The polypeptides, nucleic acids and antibodies from the present
XX CC invention are useful in the diagnosis and therapy of prostate cancer.
XX CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
XX CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
XX CC region. Prostate specific antigen (PSA) P501S was located on
XX CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
XX CC polynucleotide and polypeptide sequences used in the exemplification
XX CC of the present invention.
XX
XX SQ Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;

Query Match 97.5%; Score 472; DB 22; Length 2984;
Best Local Similarity 99.6%; Pred. No. 3.2e-113;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCTCTCTG 60
Db 2473 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCTCTG 2532
QY 61 AATTATATCTTCACTTGAATTGCAAGGATTACACATTTCACTGTGATGATATATG 120
Db 2533 AATTATATCTTCACTTGAATTGCAAGGATTACACATTTCACTGTGATGATATATG 2592

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QY 121 TGTTGC--AAAAAAGTGTCTTTTGTAAAAATTACTTGGTTTGTGAATCCATCTT 178
Db 2593 TGTTGCAAAAAAAGTGTCTTTTGTAAAAATTACTTGGTTTGTGAATCCATCTT 2652
QY 179 GCTTTTCCCATTTGGAAGTGTCTTAAACCATCTCTGAACTGGTAGAAAAACATCTGA 238
Db 2653 GCTTTTCCCATTTGGAAGTGTCTTAAACCATCTCTGAACTGGTAGAAAAACATCTGA 2712
QY 239 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTGGATGGTTCTCAGAACATTTTCACCCA 298
Db 2713 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTGGATGGTTCTCAGAACATTTTCACCCA 2772
QY 299 GACAGCCTGTTTCTATCTCTGTTTAAATAATTAATTAATTAATTAATTAATTAATTAAT 358
Db 2773 GACAGCCTGTTTCTATCTCTGTTTAAATAATTAATTAATTAATTAATTAATTAATTAAT 2832
QY 359 CCTGCTCCAATCTGCACATATAAAGTCTGTGACTTTGAAGTTTGTAGTCAGCACACCCCA 418
Db 2833 CCTGCTCCAATCTGCACATATAAAGTCTGTGACTTTGAAGTTTGTAGTCAGCACACCCCA 2892
QY 419 ACTTTATTTTCTATGCTGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCCATG 478
Db 2893 ACTTTATTTTCTATGCTGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCCATG 2952
QY 479 TCTTTTA 484
Db 2953 TCTTTTA 2958

RESULT 14
AAH02745
ID AAH02745 standard; cDNA; 2984 BP.
AC AAH02745;
XX
XX 14-JUN-2001 (first entry)
XX
XX DE Prostate tumour antigen determined cDNA sequence for P705P.
XX
XX KW Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
XX KW prostate cancer; immunogenic; cytostatic; vaccine; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200125272-A2.
XX
XX PD 12-APR-2001.
XX
XX PF 04-OCT-2000; 2000WO-US27464.
XX
XX PR 04-OCT-1999; 99US-0157455.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Xu J, Skeiky YAW, Reed SG, Cheever MA;
XX PR WPI; 2001-245062/25.
XX
XX DR P-PSDB; AAB74809.
XX
XX PT Prostate specific protein and its encoding polynucleotide, useful for
XX PT the treatment and diagnosis of prostate cancer -
XX
XX PS Claim 50; Page 219; 276pp; English.
XX
XX CC The present invention describes an isolated polypeptide (I) comprising
XX CC at least an immunogenic portion of a prostate tumour antigen protein or
XX CC its variant. (I) have cytostatic activity and can be used in vaccine
XX CC production. (I), prostate tumour antigen polynucleotides, an antigen
XX CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
XX CC pharmaceutical composition containing (I) are useful for inhibiting the
XX CC development of cancer in a patient. Antibodies specific for prostate
XX CC specific proteins and oligonucleotides that hybridise to a

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CC polynucleotide that encodes a prostate specific protein are useful
CC for detecting the presence or absence of a cancer or monitoring the
CC progression the progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
CC used in the exemplification of the present invention.

XX
SQ Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;
Query Match 97.5%; Score 472; DB 22; Length 2984;
Best Local Similarity 99.6%; Pred. No. 3.2e-113;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TTTTAAATTAAGCATTTAGTGCAGTCCCTACTGAGTACTCTTCTCTCCCTCCCTCTG 60
DB TTTTAAATTAAGCATTTAGTGCAGTCCCTACTGAGTACTCTTCTCTCCCTCCCTCTG 2532
QY 61 AATTTAATCTTTCAACTTGCATTTGCAAGGATTCACATTTTCACATGATGATATG 120
DB AATTTAATCTTTCAACTTGCATTTGCAAGGATTCACATTTTCACATGATGATATG 2592
QY 121 TGTTCG--AAAAAAGTCTCTTTGTTTAAATTAATTTGTTGTAATCCATCTT 178
DB TGTTCGCAAAAAAAGTCTCTTTGTTTAAATTAATTTGTTGTAATCCATCTT 2652
QY 179 GCTTTTCCCATTTGGAATGATTAACCCATCTCTGAACCTCTCTGAGTAAACATCTGA 238
DB GCTTTTCCCATTTGGAATGATTAACCCATCTCTGAACCTCTCTGAGTAAACATCTGA 2712
QY 239 AGAGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTTCA 298
DB AGAGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTTCA 2772
QY 299 GACAGCCTGTTTCTATCTCTTAAATTAATTTGTTGTTTAAATTAATTTGTTGTT 358
DB GACAGCCTGTTTCTATCTCTTAAATTAATTTGTTGTTTAAATTAATTTGTTGTT 2832
QY 359 CCTGCTCCCAATCTGCATATAAAGTCTGTGACTTTGAAGTTTGTAGTCAGCACCC 418
DB CCTGCTCCCAATCTGCATATAAAGTCTGTGACTTTGAAGTTTGTAGTCAGCACCC 2892
QY 419 ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACC 478
DB ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACC 2952
QY 479 TCTTTA 484
DB TCTTTA 2958

RESULT 15
AAF86953
ID AAF86953 standard; cDNA; 2984 BP.
XX
AC AAF86953;
XX
XX
DT 06-JUL-2001 (first entry)
XX
DE Human P705P inventive antigen coding sequence SEQ ID NO: 349.
XX
KW Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;
KW chromosome 11p13; zinc finger transcription factor; ss.
XX
OS Homo sapiens.
XX
PN WO200125273-A2.
XX
PD 12-APR-2001.
XX
PF 04-OCT-2000; 2000WO-US27465.
XX
PR 04-OCT-1999; 99US-0157459.
XX
PA (CORI-) CORIXA CORP.

XX Skeiky YAW, Xu J, Cheever MA, Reed SG;
PI WPI; 2001-328324/34.
XX
DR Polypeptide comprising part of the Wilm's Tumour gene product sequence is
XX used in the diagnosis and treatment of malignant diseases e.g. leukemia
XX and cancer associated with WT1 -
XX
XX Disclosure; Page 221-222; 228pp; English.
XX
CC The present invention describes compositions comprising peptides derived
CC from the Wilm's tumour protein WT1 and methods for their use in treating
CC malignant diseases. Peptides derived from both the murine and human WT1
CC proteins are provided. The human WT1 gene is found on chromosome 11p13,
CC and the protein was shown to be a zinc finger transcription factor. The
CC immunogenic peptides of the invention are particularly useful in the
CC diagnosis and treatment of cancer and leukaemia. The present sequence is
CC a coding sequence used in the exemplification of the invention.

XX
SQ Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;
Query Match 97.5%; Score 472; DB 22; Length 2984;
Best Local Similarity 99.6%; Pred. No. 3.2e-113;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TTTTAAATTAAGCATTTAGTGCAGTCCCTACTGAGTACTCTTCTCTCCCTCCCTCTG 60
DB TTTTAAATTAAGCATTTAGTGCAGTCCCTACTGAGTACTCTTCTCTCCCTCCCTCTG 2532
QY 61 AATTTAATCTTTCAACTTGCATTTTCAAGGATTCACATTTTCACATGATGATATG 120
DB AATTTAATCTTTCAACTTGCATTTTCAAGGATTCACATTTTCACATGATGATATG 2592
QY 121 TGTTCG--AAAAAAGTCTCTTTGTTTAAATTAATTTGTTGTTGTAATCCATCTT 178
DB TGTTCGCAAAAAAAGTCTCTTTGTTTAAATTAATTTGTTGTTGTAATCCATCTT 2652
QY 179 GCTTTTCCCATTTGGAATGATTAACCCATCTCTGAACCTCTCTGAGTAAACATCTGA 238
DB GCTTTTCCCATTTGGAATGATTAACCCATCTCTGAACCTCTCTGAGTAAACATCTGA 2712
QY 239 AGAGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTTCA 298
DB AGAGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTTCA 2772
QY 299 GACAGCCTGTTTCTATCTCTTAAATTAATTTGTTGTTTAAATTAATTTGTTGTT 358
DB GACAGCCTGTTTCTATCTCTTAAATTAATTTGTTGTTTAAATTAATTTGTTGTT 2832
QY 359 CCTGCTCCCAATCTGCATATAAAGTCTGTGACTTTGAAGTTTGTAGTCAGCACCC 418
DB CCTGCTCCCAATCTGCATATAAAGTCTGTGACTTTGAAGTTTGTAGTCAGCACCC 2892
QY 419 ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACC 478
DB ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACC 2952
QY 479 TCTTTA 484
DB TCTTTA 2958

Search completed: September 13, 2003, 02:00:53
Job time : 227 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 00:51:46 ; Search time 1646 Seconds
(without alignments)
7146.638 Million cell updates/sec

Title: US-09-352-616A-434

Perfect score: 484

Sequence: 1 ttttaataaagcatttagt.....ataaagtaaccatgtcttta 484

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
c 1	484	100.0	538	9	AI620178
c 2	484	100.0	663	12	BQ018482
c 3	483	99.8	661	12	BQ020946
c 4	473	97.7	599	9	AA813266

ALIGNMENTS

RESULT 1
AI620178/c
LOCUS
DEFINITION
tu54a11.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:225484 3',
mRNA sequence.
EST.
AI620178
AI620178.1 GI:4629304
EST.
Homo sapiens
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 538)
NCI-Cgap http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Sequencing by: Greg Lennon, Ph.D.
Clone Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

c 5	473	97.7	674	12	BM983868
c 6	472	97.5	631	14	CA430903
c 7	469	96.9	490	9	AA437224
c 8	447	92.4	455	9	AA972883
c 9	434	89.7	434	9	AI989281
c 10	431.4	89.1	435	9	AA809587
c 11	422	87.2	423	9	AI685682
c 12	389	80.4	607	12	BI855676
c 13	386.6	79.9	419	9	AA229495
c 14	382.8	79.1	411	9	AA640928
c 15	379	78.3	383	9	AI672753
c 16	374.2	77.3	445	9	AA533772
c 17	372	76.9	423	9	AA531606
c 18	361	74.6	377	9	AI669511
c 19	360	74.4	374	14	W47380
c 20	359	74.2	366	9	AI424280
c 21	358	74.0	386	9	AI027196
c 22	356	73.6	382	9	AA507804
c 23	356	73.6	391	10	BF511129
c 24	356	73.6	382	9	AA833543
c 25	352	72.7	380	9	AA758204
c 26	348.4	72.0	371	9	AA758204
c 27	344.4	71.2	382	9	AI692186
c 28	343.2	70.9	353	9	AA508806
c 29	332.8	68.8	354	9	AA603372
c 30	330.2	68.2	337	9	AI748915
c 31	328.8	67.9	337	9	AA400418
c 32	327	67.6	403	9	AA493522
c 33	323.2	66.8	339	9	AA650104
c 34	313.4	64.8	340	9	AA006550
c 35	304	62.8	342	9	AA228941
c 36	284.2	58.7	331	10	BF095382
c 37	278.2	57.5	311	9	AA527743
c 38	276.8	57.2	361	9	AI829793
c 39	264	54.5	472	9	AA640241
c 40	262.6	54.3	282	9	AA654919
c 41	262.4	54.2	332	10	BF508160
c 42	252	52.1	283	9	AA652376
c 43	246.6	51.0	261	9	AA650230
c 44	239	49.4	267	9	AA572913
c 45	218.6	45.2	396	12	BI360784

BM983868 UI-CF-DU1
CA430903 UI-H-FL1-
AA437224 zv54b10.s
AA972883 op24g07.s
AI989281 10. prosta
AA809587 nj4se11.s
BI855682 tt89h03.x
AA229495 nc35a03.s
AA640928 nr28d08.r
AI672753 we58d10.x
AA533772 nj39c05.s
AA531606 nj65e04.s
AI669511 w68f07.x
W47380 zc39h11.s1
AI424280 tf01g02.x
AI027196 ov83a09.x
AA507804 ng89g12.s
BF511129 UI-H-BI4-
AA833543 aj36b07.s
AA758204 ah68e11.s
AI692186 w37g02.x
AA508806 nh9c06.s
AA603372 np0ed01.s
AI748915 at28e03.x
AA400418 zu69g10.s
AA493522 ng75f05.s
AA527743 ng95e05.s
AI829793 wc07c11.x
AA640241 nr20h08.s
AA654919 nt77e01.s
BF508160 UI-H-BI4-
AA652376 ns52h09.s
AA650230 ns93e02.s
AA572913 nm42f12.s
BI360784 388827 MA

Insert Length: 825 Std Error: 0.00
Seq primer: -40Up from Gibco
High quality sequence stop: 456
POLYA=No.

FEATURES	SOURCE
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2. The third column is labeled "FEATURES".	
3. The fourth column is labeled "SOURCE".	
4. The fifth column is labeled "FEATURES".	
5. The sixth column is labeled "SOURCE".	
6. The seventh column is labeled "FEATURES".	
7. The eighth column is labeled "SOURCE".	
8. The ninth column is labeled "FEATURES".	
9. The tenth column is labeled "SOURCE".	
10. The eleventh column is labeled "FEATURES".	
11. The twelfth column is labeled "SOURCE".	
12. The thirteenth column is labeled "FEATURES".	
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15. The sixteenth column is labeled "SOURCE".	
16. The seventeenth column is labeled "FEATURES".	
17. The eighteenth column is labeled "SOURCE".	
18. The nineteenth column is labeled "FEATURES".	
19. The twentieth column is labeled "SOURCE".	
20. The twenty-first column is labeled "FEATURES".	
21. The twenty-second column is labeled "SOURCE".	
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26. The twenty-seventh column is labeled "FEATURES".	
27. The twenty-eighth column is labeled "SOURCE".	
28. The twenty-ninth column is labeled "FEATURES".	
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48. The forty-ninth column is labeled "FEATURES".	
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source
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2254844"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCL_CGAP_Pr28"
/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker; plasmid DNA from the
normalized library NCL_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."
190 a 84 c 113 q 151 t
BASE COUNT
origins

```

BASE COUNT	190 a	84 c	113 g	151 t
ORIGIN	Subtraction by Bento Soares and M. Fatima Bonaldo.			
	(17926-1220615) :			
Query Match	100.0%;	Score 484;	DB 9;	Length 538;
Best Local Similarity	100.0%;	Pred. No. 2,6e-90;		
Matches 484; Conservative	0;	Mismatches	0; Indels	0; Gaps 0;

Query Match		100.0%;	Score 484;	DB 9;	Length 538;
Best Local Similarity		100.0%;	Pred. No. 2.6e-90;		
Matches	484;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	1	TTTTAAATAAGCANTTAGTGC	TAGTCCCTACTGAGTACCTTCTCTCTCCCTCCCTCTG	60	
Db	489	TTTTAAATPACATTTAGTGC	TCASTCCCTACTGAGTACTTCTCTCCCTCCCTG	430	
Qy	61	AATTTAATCTTCAACTTGCA	ATTGCAAGGATTACACATTTTACATGTGATGATATTG	120	
Db	429	AATTTAATCTTCAACTTGCA	ATTGCAAGGATTACACATTTTACATGTGATGATATTG	370	
Qy	121	TGTTCCAAAAAAGTCTCTT	TGTTTAAAAATTACTTGGTTTGTGAATCCATCTTGC	180	
Db	369	TGTTCCAAAAAAGTCTCTT	TGTTTAAAAATTACTTGGTTTGTGAATCCATCTTGC	310	
Qy	181	TTTTTCCCAATTGGA	CTAGTCAATTAACCATCTCTGAACGTGAGAAAACATCTGAAG	240	
Db	309	TTTTTCCCAATTGGA	CTAGTCAATTAACCATCTCTGAACGTGAGAAAACATCTGAAG	250	
Qy	241	AGCTAGTCTATCAGCATCT	GACAGGGTGAATTCGATGGTCTCAGAACCATTTTCACCCAGA	300	
Db	249	AGCTAGTCTATCAGCATCT	GACAGGGTGAATTCGATGGTCTCAGAACCATTTTCACCCAGA	190	
Qy	301	CAGCCTGTTTCTATCCTG	TTTAAATAATTAGTTTGGGTTTCTCTACATGCATACAAACCC	360	
Db	189	CAGCCTGTTTCTATCCTG	TTTAAATAATTAGTTTGGGTTTCTCTACATGCATACAAACCC	130	
Qy	361	TGCTCCAATCTGTCACATA	AAAAAGTCGTGACATGAAGTTTGTAGCAGCACCCACCAAC	420	
Db	129	TGCTCCAATCTGTCACATA	AAAAAGTCGTGACATGAAGTTTGTAGCAGCACCCACCAAC	70	
Qy	421	TTTATTTTTCTATGCTG	TTTTTGGCAACATATGAGTGTGTTTGAATAAAGTACCACATGTC	480	
Db	69	TTTATTTTTCTATGCTG	TTTTTGGCAACATATGAGTGTGTTTGAATAAAGTACCACATGTC	10	
Qy	481	TTTA 484			
Db	9	TTTA 6			

RESULT 2				
BQ018482/c				
LOCUS	BQ018482	663 bp	linear	EST 27-MAR-2002
DEFINITION	UI-H-DH1-axj-l-02-0-UI.s1 NCICGAP_DHI Homo sapiens			cDNA clone
	IMAGE:5829649 3',	mRNA sequence.		
ACCESSION	BQ018482			

VERSION
KEYWORDS
SOURCE
ORGANIS

BQ018482.1 GI:19753759
EST.
Homo sapiens (human)
Homo sapiens

REFERENCE	AUTHORS	TITLE
1
2
3
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100

1 (bases 1 to 663)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute

JOURNAL
COMMENT

Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
The following repetitive elements were found in this cDNA
sequence: 1-30, >AT-rich<Flow_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes

FEATURES

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Location/Qualifiers
1. .663
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  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone IMAGE:5829649
  /tissue_type="Metastatic Chondrosarcoma"
  /dev_stage="Adult"
  /lab_host="DH10B (Life Technologies)"
  /notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site_2: Not I; NCI_CGAP_DHI is a normalized cDNA library containing the following tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCAATTCG."

```

BASE COUNT	TAG_SEQ=AGATCATTTGC"		
ORIGIN	219 a	106 c	140 g
			197 t
			1 others

Query Match	100.0%	Score 484;	DB 12;	Length 663;
Best Local Similarity	100.0%	pred. No. 2,5e-90;		
Matches 484;	Conservative	0;	Mismatches 0;	Indels 0;
Qy	1	TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG	60	
Db	510	TTTTAAATAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG	451	
Qy	61	AATTTAAATCTTTCAACTTGCATTTGCAAGGATTACACATTTTCACTGTGATGATATTG	120	
Db	450	AATTTTAATCTTTCAACTTGCATTTGCAAGGATTACACATTTTCACTGTGATGATATTG	391	
Qy	121	TGTTGCAAAAAAAGGATGCTTTGTTTAAAAATTTACTTGGTTTGCATTCATCTGTC	180	
Db	390	TGTTGCAAAAAAAGGATGCTTTGTTTAAAAATTTACTTGGTTTGCATTCATCTGTC	331	
Qy	181	TTTTTCCCCCATTTGGAACCTAGTCATTAACCCATCTCTGAATCGGTAGAAAAACATCTGAAG	240	
Db	330	TTTTTCCCCCATTTGGAACCTAGTCATTAACCCATCTCTGAATCGGTAGAAAAACATCTGAAG	271	

QY 241 AGCTAGTCTATCAGCATCTGACAGGTGAATGGATGGTCTCAGAACCAATTTACCCCGA 300
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Db 270 AGCTAGTCTATCAGCATCTGACAGGTGAATGGATGGTCTCAGAACCAATTTACCCCGA 211
|||||
QY 301 CAGCCTGTTCTATCCTCTTTAATAAATTAGTTTGGGTTCTCTACATGCATAACAAACCC 360
|||||
Db 210 CAGCCTGTTCTATCCTCTTTAATAAATTAGTTTGGGTTCTCTACATGCATAACAAACCC 151
|||||
QY 361 TGCCTCAATCTGTACATATAAAGTCTGTGACTTGAAGTTTGTAGTCAGCAGCCGCCACCAAC 420
|||||
Db 150 TGCCTCAATCTGTACATATAAAGTCTGTGACTTGAAGTTTGTAGTCAGCAGCCGCCACCAAC 91
|||||
QY 421 TTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCATGTC 480
|||||
Db 90 TTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCATGTC 31
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QY 481 TTTA 484
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Db 30 TTTA 27

RESULT 3
BQ020946/c
LOCUS BQ020946 661 bp mRNA linear EST 27-MAR-2002
DEFINITION UI-H-DHI-axh-j-06-0-UI.s1 NCI_CGAP_DHI Homo sapiens cDNA clone
IMAGE:5828837 3', mRNA sequence.
ACCESSION BQ020946
VERSION BQ020946.1 GI:19756232
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 661)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Dr. M. Bento Soares, University of Iowa
Through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
The following repetitive elements were found in this cDNA
sequence: 1-30, >AT-rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..661
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5828837"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DHI0B (Life Technologies)"
/clone_lib="NCI_CGAP_DHI"
/note="Organ: Lung; Vector: p7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_DHI is a normalized cDNA library containing the following tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The

sequence tag for this library is AGATCAATTGC.
TAG_LIB=UI-H-DHI
TAG_TISSUE=lung
TAG_SEQ=AGATCAATTGC"
BASE COUNT 220 a 106 c 139 g 194 t 2 others
ORIGIN
Query Match 99.8%; Score 483; DB 12; Length 661;
Best Local Similarity 99.8%; Pred. No. 4e-90;
Matches 483; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCCTCTG 60
|||||
Db 510 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCCTCTG 451
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QY 61 AATTAAATCTTTCAACTTGCAAATTTGCAAGATTACACATTTCACTCTGATGTATATTG 120
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Db 450 AATTAAATCTTTCAACTTGCAAATTTGCAAGATTACACATTTCACTCTGATGTATATTG 391
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QY 121 TGTTCGAAAAAAGTGTCTTTGTTTAAAAATTTACTTTGGTTTGTGAATCCATCTTGC 180
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Db 390 TGTTCGAAAAAAGTGTCTTTGTTTAAAAATTTACTTTGGTTTGTGAATCCATCTTGC 331
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QY 181 TTTTCCCATTTGGAATAGTACATTAACCCATCTCTGAACCTGTGAGTGTAGAAAAACATCTGAAG 240
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|||||
QY 301 CAGCCTGTTCTATCCTCTTTAATAAATTAGTTTGGGTTCTCTACATGCATAACAAACCC 360
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Db 210 CAGCCTGTTCTATCCTCTTTAATAAATTAGTTTGGGTTCTCTACATGCATAACAAACCC 151
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QY 361 TGCCTCAATCTGTACATATAAAGTCTGTGACTTGAAGTTTGTAGTCAGCAGCCGCCACCAAC 420
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Db 150 TGCCTCAATCTGTACATATAAAGTCTGTGACTTGAAGTTTGTAGTCAGCAGCCGCCACCAAC 91
|||||
QY 421 TTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCATGTC 480
|||||
Db 90 TTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCATGTC 31
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QY 481 TTTA 484
|||||
Db 30 TTTA 27

AA813266 599 bp mRNA linear EST 31-DEC-1998
aj44903.s1 Soares_testis_NHT Homo sapiens cDNA clone 1393204 3',
mRNA sequence.
ACCESSION AA813266
VERSION AA813266.1 GI:2883251
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 599)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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Seq primer: -40ml3 fwd. Et from Amersham
High quality sequence stop: 503.
Location/Qualifiers

FEATURES

source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1393204"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares_testis_NHT"
/note="Vector: pT73-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - oligo(dT) primer [5].
TGTACCAATCTGAAGTGGAGCGCCCAATTTTTTTTTTTT 3].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."
202 a 98 c 131 g 168 t

BASE COUNT

ORIGIN

Query Match 97.7%; Score 473; DB 9; Length 599;
Best Local Similarity 99.8%; Pred. No. 4.9e-88;
Matches 484; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TTTTAAATAAGCATTAGTGCTCAGTCCCTACTGAGTACTCTTTCTCCCTCCTCTG 60
DB 493 TTTTAAATAAGCATTAGTGCTCAGTCCCTACTGAGTACTCTTTCTCCCTCCTCTG 434
QY 61 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATG 120
DB 433 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATG 374
QY 121 TGTGTC-AAAAAAGAGTCTTTGTTTAAATTAATTTGTTTGAATTCCTGATATATG 179
DB 373 TGTGTC-AAAAAAGAGTCTTTGTTTAAATTAATTTGTTTGAATTCCTGATATATG 314
QY 180 CTTTTCCTCCATGGAACATGATTAACCCATCTCTGAACCTGAGTAAACATCTGAA 239
DB 313 CTTTTCCTCCATGGAACATGATTAACCCATCTCTGAACCTGAGTAAACATCTGAA 254
QY 240 GAGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTACCCAG 299
DB 253 GAGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTACCCAG 194
QY 300 ACAGCCTGTTCTATCTCTGTTTAAATTAATTTGTTTGGTTCCTACATGCATACAAACC 359
DB 193 ACAGCCTGTTCTATCTCTGTTTAAATTAATTTGTTTGGTTCCTACATGCATACAAACC 134
QY 360 CTGCTCCAATCTGCACATAAAGTCTGACTTGAAGTTAGTCAGCAGCCCAACAAA 419
DB 133 CTGCTCCAATCTGCACATAAAGTCTGACTTGAAGTTAGTCAGCAGCCCAACAAA 74
QY 420 CTTTATTTCTATGTTGTTTTCACATATGAGTGTGTTTGAATTAATTAATTAATTAAT 479
DB 73 CTTTATTTCTATGTTGTTTTCACATATGAGTGTGTTTGAATTAATTAATTAATTAAT 14
QY 480 CTTTA 484
DB 13 CTTTA 9

RESULT 5

BM983868/c

LOCUS

DEFINITION 674 bp mRNA linear EST 20-FEB-2003
UI-CF-DUI1-aaw-b-04-0-UI.s1 UI-CF-DUI1 Homo sapiens cDNA clone

ACCESSION BM983868

VERSION
KEYWORDS
SOURCE
ORGANISM

BM983868.1 GI:19608810

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 674)

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com) or from Open Biosystems

(www.openbiosystems.com).

The following repetitive elements were found in this cDNA

sequence: 1-21, >AT-rich#Low_complexity (matched complement)

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..674

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-CF-DUI1-aaw-b-04-0-UI"

/tissue_type="Primary Lung Epithelial Cells"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-CF-DUI"

/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-DUI1 is a normalized cDNA library containing the
following tissue(s): Primary Lung Epithelial Cells The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT73-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is GCGTGTAGGC.
TAG_LIB=UI-CF-DUI

TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368

TAG_SEQ=GGCTGTAGGC"

BASE COUNT 221 a 111 c 144 g 198 t

ORIGIN

Query Match

Best Local Similarity 99.8%; Score 473; DB 12; Length 674;

Matches 484; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TTTTAAATAAGCATTAGTGCTCAGTCCCTACTGAGTACTCTTTCTCCCTCCTCTG 60
DB 502 TTTTAAATAAGCATTAGTGCTCAGTCCCTACTGAGTACTCTTTCTCCCTCCTCTG 443
QY 61 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATG 120
DB 442 AATTAAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATATATG 383

```
Qy 121 TGTTCGCAAAAAAAGTGTCTTTGTTAAATTAATCTGGTTGTGAATCCATCTTGC 180
Db 382 TGTTCGCAAAAAAAGTGTCTTTGTTAAATTAATCTGGTTGTGAATCCATCTTGC 323
Qy 181 TTTTCCCATGGAACCTAGTCATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAG 240
Db 322 TTTTCCCATGGAACCTAGTCATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAG 263
Qy 241 AGCTAGTCTATCAGCATCTGACAGGTGAATGGATGTTCTCTCAGAACCATTTCACCCAGA 300
Db 262 AGCTAGTCTATCAGCATCTGACAGGTGAATGGATGTTCTCTCAGAACCATTTCACCCAGA 203
Qy 301 CAGCCTGTTCTATCCCTGTTTATAAATTAATAGTTGGGTTCTCTACATGATCAATAACCC 360
Db 202 CAGCCTGTTCTATCCCTGTTTATAAATTAATAGTTGGGTTCTCTACATGATCAATAACCC 143
Qy 361 TGTCCCAATCTGCACATAAAGCTGTGACTTCAAGTCTAGTCAAGCAGCCCA-CCAAA 419
Db 142 TGTCCCAATCTGCACATAAAGCTGTGACTTCAAGTCTAGTCAAGCAGCCCA-CCAAA 83
Qy 420 CTTTATTTTCTATGTTGTTTTCGCAACATATGAGTGTGTTTGAATAAAGTACCCATGT 479
Db 82 CTTTATTTTCTATGTTGTTTTCGCAACATATGAGTGTGTTTGAATAAAGTACCCATGT 23
Qy 480 CTTTA 484
Db 22 CTTTA 18
```

RESULT 6

```
CA430903/c
LOCUS CA430903 631 bp mRNA linear EST 07-NOV-2002
DEFINITION UI-H-FL1-bge-i-17-0-UI.s1 NCI CGAP FL1 Homo sapiens cDNA clone
            UI-H-FL1-bge-i-17-0-UI 3', mRNA sequence.
VERSION CA430903
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 631)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
        Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
        Email: cgapbs-r@mail.nih.gov
        Tissue Procurement: James Martin
        cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
        DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
        Clone Distribution: Clone distribution information can be obtained
        from Dr. M. Bento Soares, bento-soares@uiowa.edu
        Seq primer: M13 FORWARD
        POLYA=Yes.
```

FEATURES

source

```
RESULT 7
LOCUS AA437224/c
DEFINITION zV54b10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757435
            3' similar to contains Alu repetitive element.; mRNA sequence.
ACCESSION AA437224
VERSION AA437224.1 GI:2142138
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 490)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
        Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
        Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, X., Wylie,
        T., Waterston, R. and Willson, R.
```

with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GAGTCCGGTG. The cell lines were provided by Dr. James Martin from the University of Iowa.

TAG_LIB=UI-H-FL1
TAG_TISSUE=Human Chondrosarcoma Grade 3 cell line mix
TAG_SEQ=GAGTCCGGTG

BASE COUNT 210 a 102 c 136 g 182 t 1 others
ORIGIN

Query Match 97.5%; Score 472; DB 14; Length 631;

Best Local Similarity 99.8%; Pred. No. 7.8e-88;

Matches 483; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy 1 TTTTAAATAGCAATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCCCTCTGTG 60
Db 505 TTTTAAATAGCAATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCCCTCTGTG 446
Qy 61 AATTTAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGTATATTG 120
Db 445 AA-TTAATCTTCAACTTGCATTTGCAAGGATTACACATTTCACTGTGATGTATATTG 387
Qy 121 TGTTCGCAAAAAAAGTGTCTTTGTTTAAATTAATCTGGTTGTGAATCCATCTTGC 180
Db 386 TGTTCGCAAAAAAAGTGTCTTTGTTTAAATTAATCTGGTTGTGAATCCATCTTGC 327
Qy 181 TTTTCCCATGGAACCTAGTCATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAG 240
Db 326 TTTTCCCATGGAACCTAGTCATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGAAG 267
Qy 241 AGCTAGTCTATCAGCATCTGACAGGTGAATGGATGTTCTCAGAACCATTTCACCCAGA 300
Db 266 AGCTAGTCTATCAGCATCTGACAGGTGAATGGATGTTCTCAGAACCATTTCACCCAGA 207
Qy 301 CAGCCTGTTCTATCCCTGTTTAAATTAATAGTTGGTTCCTCATGATCAATAACACCC 360
Db 206 CAGCCTGTTCTATCCCTGTTTAAATTAATAGTTGGTTCCTCATGATCAATAACACCC 147
Qy 361 TGTCCCAATCTGCACATAAAGTCTGTGACTTGAAGTTTGTAGTCAGCAGCCCAACAC 420
Db 146 TGTCCCAATCTGCACATAAAGTCTGTGACTTGAAGTTTGTAGTCAGCAGCCCAACAC 87
Qy 421 TTTATTTTCTATCTGTTTGTGCAACATATGAGTGTGTTGAAAATAAAGTACCCATGTC 480
Db 86 TTTATTTTCTATCTGTTTGTGCAACATATGAGTGTGTTGAAAATAAAGTACCCATGTC 27
Qy 481 TTTTA 484
Db 26 TTTTA 23
```



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QY 338 TTCTCTACATGATCAAAACCCCTGCTCCCAATCTGTCCACATAAAAGTCTGTGACTTGAAG 397
|||||
Db 155 TTCTCTACATGATCAAAACCCCTGCTCCCAATCTGTCCACATAAAAGTCTGTGACTTGAAG 96
|||||
QY 398 TTTAGTCAGCAGCCCCACCAAACTTTATTTTCTATGTGTTTTTTCACAATATGAGTGT 457
|||||
Db 95 TTTAGTCAGCAGCCCCACCAAACTTTATTTTCTATGTGTTTTTTCACAATATGAGTGT 36
|||||
QY 458 TTTGAAATAAAGTACCATGCTTTTA 484
|||||
Db 35 TTTGAAATAAAGTACCATGCTTTTA 9
|||||

RESULT 9
AI989281 434 bp mRNA linear EST 02-SEP-2001
LOCUS 10 prostate cancer cell line LNCap Homo sapiens cDNA, mRNA
DEFINITION
ACCESSION AI989281
VERSION AI989281.1 GI:15421029
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 434)
AUTHORS Zhang, J.S. and Smith, D.I.
TITLE High throughput screening for androgen regulated genes in LNCap
cells: identification of Hsp-2 as an androgen regulated gene over
expressed in prostate adenocarcinoma
JOURNAL Unpublished
COMMENT Contact: Zhang, Jin-San
Dept. Pathology and Lab Medicine
Mayo Clinic Cancer Center
200 1st St. SW, Rochester MN 55905, USA
Tel: 507-2660311
Fax: 507-2665193
Email: zhang.jinsan@mayo.edu.

FEATURES
Location/Qualifiers
source 1..434
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="LNCap"
/clone_lib="prostate cancer cell line LNCap"
/notes="prostate cancer metastasized to lymph node;
subtracted cDNA libraries from prostate cancer cell line
LNCap treated with androgen."
BASE COUNT 123 a 91 c 66 g 154 t
ORIGIN

Query Match 89.7%; Score 434; DB 9; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.3e-80;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 CTCTTTCTCCCTCCTCGAATTAATTTCACTTGCATTTGCAAGTATACAC 99
|||||
Db 1 CTCTTTCTCCCTCCTCGAATTAATTTCACTTGCATTTGCAAGTATACAC 60
|||||
QY 100 ATTTCACTGTGATGATATGTTGTGCAAAAAAAGTGTCTTTGTTTAAATPACT 159
|||||
Db 61 ATTTCACTGTGATGATATGTTGTGCAAAAAAAGTGTCTTTGTTTAAATPACT 120
|||||
QY 160 TGCTTTGTGAATCCATCTTCTTTTCCCATTTGGAAGTACTGATTAACCCATCTCGAA 219
|||||
Db 121 TGGTTGTGAATCCATCTTCTTTTCCCATTTGGAAGTACTGATTAACCCATCTCGAA 180
|||||
QY 220 CTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGATGGTT 279
|||||
Db 181 CTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGATGGTT 240
|||||
QY 280 CTCAGAACCAATTTTACCACAGACAGCCCTGTTTCTATCTCTGTTTAAATAAATTAGTTGGTT 339
|||||

Db 241 CTCAGAACCAATTTTACCACAGACAGCCCTGTTTCTATCTCTGTTTAAATAAATTAGTTGGTT 300
|||||
QY 340 CTCTACATGATACAAACCCCTGCTCCCAATCTGTCCACATAAAAGTCTGTGACTTGAAGTT 399
|||||
Db 301 CTCTACATGATACAAACCCCTGCTCCCAATCTGTCCACATAAAAGTCTGTGACTTGAAGTT 360
|||||
QY 400 TAGTCAGCAGCCCCACCAAACTTTATTTTCTATGTGTTTTTTCACAATATGAGTGT 459
|||||
Db 361 TAGTCAGCAGCCCCACCAAACTTTATTTTCTATGTGTTTTTTCACAATATGAGTGT 420
|||||
QY 460 TGAATAAAGTAC 473
|||||
Db 421 TGAATAAAGTAC 434
|||||

RESULT 10
AA809587 435 bp mRNA linear EST 18-FEB-1998
LOCUS n743ell.s1 NCI_CGAP_Pr9 Homo sapiens cDNA clone IMAGE:995276, mRNA
DEFINITION
ACCESSION AA809587
VERSION AA809587.1 GI:2878993
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-re@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 605 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.

FEATURES
Location/Qualifiers
source 1..435
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:995276"
/sex="male"
/tissue_type="normal prostatic epithelial cells"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr9"
/notes="Organ: prostate; Vector: pAMP10; mRNA made from
normal prostatic epithelial cells, cDNA made by oligo-dT
priming. Non-directionally cloned. Size-selected on
agarose gel, average insert size 600 bp. Library made by
D. Krizman, NIH."
BASE COUNT 120 a 96 c 68 g 151 t
ORIGIN

Query Match 89.1%; Score 431.4; DB 9; Length 435;
Best Local Similarity 99.8%; Pred. No. 2.2e-79;
Matches 432; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 22 CTCAGTCCCCTACTGAGTACTCTTCTCTCCCTCTCTGAATTAATTTCTTCAACTGC 81
|||||
Db 3 CTCAGTCCCCTACTGAGTACTCTTCTCTCCCTCTCTGAATTAATTTCTTCAACTGC 62
|||||
QY 82 AATTTGCAAGGATTACACATTTTCACTGTGATGATATGTTGTGCAAAAAAAGT 141
|||||
```

Db 63 AATTGCAAGATTACACATTTCACTGTGATGATATATGTGTTGCAAAAAAAGAGTG 122

QY 142 TCTTTGTTTAAATTAATCTGTTTGTGAATCCATCTTGCTTTTCCCATTTGGAACATAGT 201

Db 123 TCTTTGTTTAAATTAATCTGTTTGTGAATCCATCTTGCTTTTCCCATTTGGAACATAGT 182

QY 202 CATTAAACCCATCTGTAACCTGGTAGAATAACATCTGAAGAGCTAGTCTATFAGCATCTGA 261

Db 183 CATTAAACCCATCTGTAACCTGGTAGAATAACATCTGAAGAGCTAGTCTATFAGCATCTGA 242

QY 262 CAGGTGAATTTGGATGTTCTCAGAACCATTTACCCAGACAGCTGTTCTATCCGTTT 321

Db 243 CAGGTGAATTTGGATGTTCTCAGAACCATTTACCCAGACAGCTGTTCTATCCGTTT 302

QY 322 AATAAATAGTTTGGGTTCTCATATGCATACATAACAAACCCCTGCTCCAACTGTGCACATAAA 381

Db 303 AATAAATAGTTTGGGTTCTCATATGCATACATAACAAACCCCTGCTCCAACTGTGCACATAAA 362

QY 382 AGTCTGTGACTTCAAGTTTAGTCAGACACCCACCAACCAACTTTATTTTCTATGTGTTTTT 441

Db 363 AGTCTGTGACTTCAAGTTTAGTCAGACACCCACCAACCAACTTTATTTTCTATGTGTTTTT 422

QY 442 TGCACATATGAG 454

Db 423 TGCACATATGAG 435

RESULT 11

AI685682/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AI685682

tt89h03.x1 NCI_CGAP_Pr28 423 bp mRNA linear EST:27-MAY-1999

mRNA sequence.

AI685682.1 GI:4896976

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -400P from Gibco.

Location/Qualifiers

1. 423

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2248757"

/sex="male"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonids 985608-986759, 1101192-1101959, and 1217928-1220615).

BASE COUNT 150 a 66 c 83 g 124 t

ORIGIN

Query Match 87.2%; Score 422; DB 9; Length 423;

Best Local Similarity 100.0%; Pred. No. 1.9e-77;

Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 TTTAATCTTTCAACTTGCATTTCAAGGATTACACATTTCACTGTGATGATGTTG 122

Db 423 TTTAATCTTTCAACTTGCATTTCAAGGATTACACATTTCACTGTGATGATGTTG 364

QY 123 TTGCAAAAAAAGAGTCTCTTTTAAATTAATCTGTTTGAATCCATCTGCTT 182

Db 363 TTGCAAAAAAAGAGTCTCTTTTAAATTAATCTGTTTGAATCCATCTGCTT 304

QY 183 TTTCCCATTTGAATAGTCTATTAACCATCTCTGAAGTGTGAGAAACATCTGAAGAG 242

Db 303 TTTCCCATTTGAATAGTCTATTAACCATCTCTGAAGTGTGAGAAACATCTGAAGAG 244

QY 243 CTAGTCTATCAGCATCTCAGAGGTGAATTTGGATGTTCTCAGAACCATTTTCAACCCAGACA 302

Db 243 CTAGTCTATCAGCATCTCAGAGGTGAATTTGGATGTTCTCAGAACCATTTTCAACCCAGACA 184

QY 303 GCCTGTTTCTATCTCTGTTTAAATTAATTAATTTGGGTTCTCTACATGATACAAACCTG 362

Db 183 GCCTGTTTCTATCTCTGTTTAAATTAATTAATTTGGGTTCTCTACATGATACAAACCTG 124

QY 363 CTCCAATCTGTACATATAAAGTCTGTGACTTGAAGTTTAGTCAGCAGCCCAACCAACTT 422

Db 123 CTCCAATCTGTACATATAAAGTCTGTGACTTGAAGTTTAGTCAGCAGCCCAACCAACTT 64

QY 423 TATTTTCTATGTTGTTTTCGACATATGAGTCTTTTGAATAAAGTACCACTGCTT 482

Db 63 TATTTTCTATGTTGTTTTCGACATATGAGTCTTTTGAATAAAGTACCACTGCTT 4

QY 483 TA 484

Db 3 TA 2

RESULT 12

BI855676/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BI855676

603383205F2 NIH_MGC_87 Homo sapiens CDNA clone IMAGE:5392201 5', mRNA sequence.

BI855676

BI855676.1 GI:15996423

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DMP

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM1999 row: i column: 02

High quality sequence stop: 586.

Location/Qualifiers

1. 607

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

FEATURES

source

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/clone="IMAGE:5392201"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC.87"
/clone="Organ: breast; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT      215 a      86 c      139 g      167 t
ORIGIN

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Query Match      80.4%; Score 389; DB 12; Length 607;
Best Local Similarity 96.6%; Pred. No. 1.3e-70;
Matches 451; Conservative 0; Mismatches 10; Indels 6; Gaps 5;

QY 20 TGCACAGCCCTACTGAGTACTCTTCTCTCCCTCCCTCTGAATTAATTTCTTCAACTT 79
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 469 TCCACAGCCCTACTGAGTACTCTTCTCTCCCTCCCTCTGAATTAATTTCTTCCACTT 410
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 80 GCAATTTGCA-AGGATTACACATTTCACTGTGATGTATATTGTGTG-CAAAAAATAAAA 137
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 409 GCCATTGCACAGGATTACACATTTCACTGTGAAGTATATTGTGTGCCAAAAAATAAAA 350
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 138 AGTGCTTTGTTTAAATTAATTTGTTGTGAATCCATCTTGCTTTTCCCATTTGGAAC 197
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 349 AGTGCTTTGTTTAAATTAATTTGTTGTGAATCCATCTTGCTTTTCCCATTTGGAAC 290
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 198 TAGTCATTAACCCATCTGAACTGGTGTAGAAAAACATCTGAAGACTAGTCTATCAGCAT 257
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 289 TAGTCATTAACCCATCTGAACTGGTGTAGAAAAACATCTGAAGACTAGTCTATCAGCAT 230
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 258 CTGACAGGTGAATTTGATGGTTCTCAGAACCATTTACCCAGACAGCCCTGTTCTATCCT 317
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 229 CTGACAGGTGAATTTGATGGTTCTCAGAACCATTTACCCAGACAGCCCTGTTCTATCCT 170
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 318 GTTTAATAAATVAGTTGGTGTCTACATGCATAAACAACCCCTGCTCCAATCTGTCACA 377
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 169 GTTTAATAAATVAGTTGGTGTCTACATGCATAAACAACCCCTGCTCCAATCTGTCACA 112
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 378 TAAAGTCTGTGACTTGAAGTTTGTAGTACAGACCCCAACCAACTTATTTTCTATGTGT 437
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 111 TAAAGTCTGTGACTTGAAGTTTGTAGTACAGACCCCAACCAACTTATTTTCTATGTGT 53
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 438 TTTTGGCAACATATGAGTGTGTTTGAATAAAGTACCCATGCTCTTTA 484
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 52 TTTTGG-ACATATGAGTGTGTTTGAATAAAGTACCCATGCTCTTTA 7
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 13
AA229495/c
LOCUS      AA229495      419 bp      mRNA      linear      EST 21-AUG-1997
DEFINITION nc35a03.s1 NCI_CGAP_pr2 Homo sapiens cDNA clone IMAGE:1010092
            similar to contains Alu repetitive element; mRNA sequence.
ACCESSION  AA229495
VERSION     1
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 419)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished
CONTACT     Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
            , Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

```

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 856 Std Error: 0.00

Seq Primer: 41ml3 fwd. ET from Amersham

High quality sequence stop: 368.

FEATURES

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Location/Qualifiers
1..419
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:1010092"
    /sex="Male"
    /dev_stage="45 years old"
    /lab_host="DH10B"
    /clone_lib="NCI_CGAP_Pr2"
    /note="Vector: PAMP10; Site_1: NotI; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from 5,000-10
,000 microdissected preneoplastic cells
histologically-determined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
BASE COUNT      141 a      68 c      79 g      131 t
ORIGIN

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Query Match      79.9%; Score 386.6; DB 9; Length 419;
Best Local Similarity 98.5%; Pred. No. 4.3e-70;
Matches 401; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

QY 80 GCAATTTGCAAGGATTACACATTTTCACCTGTGATGTATATTGTGTGTC--AAAAAATAAAA 137
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 419 GCAATTTGCAAGGATTACACATTTTCACCTGTGATGTATATTGTGTGTCAAAAAATAAAA 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 138 AGTGCTTTGTTTAAATTAATTTGTTGTGAATCCATCTTGCTTTTCCCATTTGGAAC 197
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 359 AGTGCTTTGTTTAAATTAATTTGTTGTGAATCCATCTTGCTTTTCCCATTTGGAAC 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 198 TAGTCATTAACCCATCTGAACTGGTGTAGAAAAACATCTGAAGACTAGTCTATCAGCAT 257
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 299 TAGTCATTAACCCATCTGAACTGGTGTAGAAAAACATCTGAAGACTAGTCTATCAGCAT 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 258 CTGACAGGTGAATTTGATGGTTCTCAGAACCATTTACCCAGACAGCCCTGTTTCTATCCT 317
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 239 CTGACAGGTGAATTTGATGGTTCTCAGAACCATTTACCCAGACAGCCCTGTTTCTATCCT 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 318 GTTTAATAAATVAGTTGGTGTCTACATGCATAAACAACCCCTGCTCCAATCTGTCACA 377
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 179 GTTTAATAAATVAGTTGGTGTCTACATGCATAAACAACCCCTGCTCCAATCTGTCACA 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 378 TAAAGTCTGTGACTTGAAGTTTGTAGTACAGACCCCAACCAACTTATTTTCTATGTGT 437
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 119 TAAAGTCTGTGACTTGAAGTTTGTAGTACAGACCCCAACCAACTTATTTTCTATGTGT 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 438 TTTTGGCAACATATGAGTGTGTTTGAATAAAGTACCCATGCTCTTTA 484
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 59 TTTTGGCAACATATGAGTGTGTTTGAATAAAGTACCCAGGCTCTTTA 13
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 14
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LOCUS      AA640928      411 bp      mRNA      linear      EST 27-OCT-1997
DEFINITION nr28d08.r1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1169295, mRNA
            sequence.
ACCESSION  AA640928
VERSION     AA640928.1
KEYWORDS   EST.
SOURCE      Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 411)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.
Clone distribution: Washington University Genome Sequencing Center
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Seq primer: -28m13 revl Et from Amersham
High quality sequence stop: 387.
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source
Location/Qualifiers
1..411
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1169295"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/clone_lib="NCI-CGAP_Pr3"
/note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
BASE COUNT 123 a 80 c 68 g 140 t
ORIGIN
Query Match 79.1%; Score 382.8; DB 9; Length 411;
Best Local Similarity 99.2%; Pred. No. 2.6e-69;
Matches 395; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 88 CAAGGATTACACATTTCACTGTCATGTATATTGTGTGC-AAAAAAAAAAAGTGCTTT 146
DB 5 CAAGGATTACACATTTCACTGTCATGTATATTGTGTGC-AAAAAAAAAAAGTGCTTT 64
QY 147 GTTTAAATTAAGTTGTTGTAATCCATCTTGTCTTTTCCCATTTGGAAGTCTCATT 206
DB 65 GTTTAAATTAAGTTGTTGTAATCCATCTTGTCTTTTCCCATTTGGAAGTCTCATT 124
QY 207 ACCCATCTCTGAACCTGGTAGAACAATCTGAAGAGCTAGTCTATCAGCATCTGACAGT 266
DB 125 ACCCATCTCTGAACCTGGTAGAACAATCTGAAGAGCTAGTCTATCAGCATCTGACAGT 184
QY 267 GAATTGGATGGTCTCAGAACCATTTACCCAGACAGCCTGTTTCTATCTGTTTAAATA 326
DB 185 GAATTGGATGGTCTCAGAACCATTTACCCAGACAGCCTGTTTCTATCTGTTTAAATA 244
QY 327 ATTAGTTTGGTCTCTACATGCATACAAACCCCTGCTCCAAATCTGTCACATAAAGTCT 386
DB 245 ATTAGTTTGGTCTCTACATGCATACAAACCCCTGCTCCAAATCTGTCACATAAAGTCT 304
QY 387 GTGACTTGAAGTTTAGTCAGCACCCGCCCAAACTTTATTTTCTATGTTGTTTTCGAA 446
DB 305 GTGACTTGAAGTTTAGTCAGCACCCGCCCAAACTTTATTTTCTATGTTGTTTTCGAA 364
QY 447 CATATGAGTGTTTGAAATAAAGTACCCATGCTTTTA 484

Db 365 CATATGAGTGTTTGAAATAAGTACCCATGCTTTA 402
RESULT 15
LOCUS AI672753 383 bp mRNA linear EST 18-DEC-1999
DEFINITION we58d10.x1 Soares thymus NHPT Homo sapiens cDNA clone IMAGE:2345299 3' similar to contains Alu repetitive element; mRNA sequence.
ACCESSION AI672753
VERSION AI672753.1 GI:4852484
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 383)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1465 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 362.
FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2345299"
/dev_stage="fetal"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Soares_thymus_NHPT"
/note="Organ: thymus, pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGTGGAGCGCGCGCAAGCTTTTCTTTTCTTTTCTTTT 3']
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 134 a 63 c 75 g 111 t
ORIGIN
Query Match 78.3%; Score 379; DB 9; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.6e-68;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 106 CTGTATGTATATTGTTGTGCAAAAAAAGTGTCTTTGTTTAAATTTACTTGGTT 165
DB 383 CTGTATGTATATTGTTGTGCAAAAAAAGTGTCTTTGTTTAAATTTACTTGGTT 324
QY 166 GTGAATCCATCTTGTCTTTTCCCATTTGGAAGTCTGATTAACCCATCTCTGAAGT 225
DB 323 GTGAATCCATCTTGTCTTTTCCCATTTGGAAGTCTGATTAACCCATCTCTGAAGT 264
QY 226 GAAATAATCTGAAGAGCTAGTCTATCAGCATCTGCAGGTGAATTTGATGGTCTCAGA 285
DB 263 GAAATAATCTGAAGAGCTAGTCTATCAGCATCTGCAGGTGAATTTGATGGTCTCAGA 204
QY 286 ACCATTTTCAACCCAGACAGCTGTTTCTATCTCTTTTAAATAGTTGGTGTCTCTAC 345
DB 203 ACCATTTTCAACCCAGACAGCTGTTTCTATCTCTTTTAAATAGTTGGTGTCTCTAC 144
QY 346 ATGCATAACAACCCCTCTCCAATCTGTCAATAAAGTCTGAGCTTGAAGTTAGTCA 405

Db 143 ATGCATAACAAACCCGTCTCCAATCTGTCTACATAAAAGTCTGTGACTTTGAAGTTTAGTCA 84
Qy 406 GCACCCCCACCAAACTTTATTTTCTCTATGTGTGTTTTTTGCAACATATGAGTGTGTTTTGAAAA 465
Db 83 GCACCCCCACCAAACTTTATTTTCTCTATGTGTGTTTTTTGCAACATATGAGTGTGTTTTGAAAA 24
Qy 466 TAAAGTACCATGCTCTTTA 484
Db 23 TAAAGTACCATGCTCTTTA 5

Search completed: September 13, 2003, 02:28:29
Job time : 1651 secs

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OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 01:51:10 ; Search time 55 Seconds
(without alignments)
3884.172 Million cell updates/sec

Title: US-09-352-616A-434

Perfect score: 484
Sequence: 1 ttttaataaagcatttagt.....ataaagtaccatgtcttta 484

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	484	100.0	484	US-09-439-313-434	Sequence 434, App
2	484	100.0	484	US-09-352-616A-434	Sequence 434, App
3	472	97.5	2051	US-09-328-475C-334	Sequence 334, App
4	472	97.5	2984	US-09-439-313-335	Sequence 335, App
5	472	97.5	2984	US-09-352-616A-335	Sequence 335, App
6	472	97.5	2984	US-09-232-149A-335	Sequence 335, App
7	426.2	88.1	1020	US-09-328-475C-102	Sequence 102, App
8	426.2	88.1	1021	US-09-328-475C-103	Sequence 103, App
9	415.6	85.9	822	US-09-328-475C-223	Sequence 223, App
10	382.8	79.1	497	US-09-328-475C-222	Sequence 222, App
11	365	75.4	366	US-09-020-956-115	Sequence 115, App
12	365	75.4	366	US-09-030-607-115	Sequence 115, App
13	365	75.4	366	US-09-439-313-115	Sequence 115, App
14	365	75.4	366	US-09-352-616A-115	Sequence 115, App
15	365	75.4	366	US-09-232-149A-115	Sequence 115, App
16	332	68.6	335	US-09-020-956-141	Sequence 141, App
17	332	68.6	335	US-09-030-607-141	Sequence 141, App
18	332	68.6	335	US-09-439-313-141	Sequence 141, App
19	332	68.6	335	US-09-352-616A-141	Sequence 141, App
20	332	68.6	335	US-09-232-149A-141	Sequence 141, App
21	305.6	63.1	317	US-09-439-313-453	Sequence 453, App
22	305.6	63.1	317	US-09-352-616A-453	Sequence 453, App
23	292.6	60.5	305	US-09-439-313-295	Sequence 295, App
24	292.6	60.5	305	US-09-352-616A-295	Sequence 295, App
25	292.6	60.5	305	US-09-232-149A-295	Sequence 295, App
26	181	37.4	181	US-09-222-575-33	Sequence 33, Appl
27	181	37.4	181	US-09-389-681-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-09-439-313-434
; Sequence 434, Application US/09439313
; Patent No. 6329505

GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jiang Yuqi

; APPLICANT: Reed, Steven G.

; APPLICANT: Kalos, Michael

; APPLICANT: Fanger, Gary

; APPLICANT: Retter, Mark

; APPLICANT: Solk, John

; APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C9

; CURRENT APPLICATION NUMBER: US/09/439,313

; CURRENT FILING DATE: 1999-11-12

; NUMBER OF SEQ ID NOS: 575

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 434

; LENGTH: 484

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-439-313-434

Query Match 100.0%; Score 484; DB 4; Length 484;

Best Local Similarity 100.0%; Pred. No. 6.5e-121; Mismatches 0; Indels 0; Gaps 0;

Matches 484; Conservative 0; Indels 0; Gaps 0;

QY 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 60

Db 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 60

QY 61 AATTAATTTCTTCAACTTGAACCTGCAATTTGCAAGGATTACACATTTCACTGTGATGATATG 120

Db 61 AATTAATTTCTTCAACTTGAACCTGCAATTTGCAAGGATTACACATTTCACTGTGATGATATG 120

QY 121 TGTTCGCAAAAAAAGAGTCTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTTGC 180

Db 121 TGTTCGCAAAAAAAGAGTCTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTTGC 180

QY 181 TTTTTCCTCCATTGGAACCTAGTCTTAACCCATCTCTGAACTGGTGAAGAAACATCTGGAAG 240

Db 181 TTTTTCCTCCATTGGAACCTAGTCTTAACCCATCTCTGAACTGGTGAAGAAACATCTGGAAG 240

QY 241 AGCTAGTCTATCAGCATCTGACAGGTGAATGGATGTTCTCAGAACCATTTCAACCCAGA 300

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Db 301 CAGCCTGTTTCTATCTGTTTAAATAAATTAGTTGGGTCTCTACATGCATAACAACCC 360
QY 361 TGCCTCAATCTGCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACCAAC 420
Db 361 TGCCTCAATCTGCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACCAAC 420
QY 421 TTTATTTTCTATGTTGTTTTTGCACATATGAGTGTGTTTTGAAAAATAAAGTACCCATGTC 480
Db 421 TTTATTTTCTATGTTGTTTTTGCACATATGAGTGTGTTTTGAAAAATAAAGTACCCATGTC 480
QY 481 TTTA 484
Db 481 TTTA 484

RESULT 2
US-09-352-616A-434
; Sequence 434, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 434
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616A-434
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Best Local Similarity 100.0%; Pred. No. 6.5e-121;
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 60
QY 61 AATTTAAATCTTCAACTTGCAATTTGCAAGGATTACACATTTCACTCTGTATATATG 120
Db 61 AATTTAAATCTTCAACTTGCAATTTGCAAGGATTACACATTTCACTCTGTATATATG 120
QY 121 TGTGCAAAAAAAGTGTCTTTGTTTAAATTAATTTACTTGGTTGTAATCCATCTGC 180
Db 121 TGTGCAAAAAAAGTGTCTTTGTTTAAATTAATTTACTTGGTTGTAATCCATCTGC 180
QY 181 TTTTCCCATTTGGAACCTAGTCATTAAACCCATCTCTGAACCTGTAGAAAAACATCTGA 240
Db 181 TTTTCCCATTTGGAACCTAGTCATTAAACCCATCTCTGAACCTGTAGAAAAACATCTGA 240
QY 241 AGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTCAACCCAGA 300
Db 241 AGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTCAACCCAGA 300
QY 301 CAGCCTGTTTCTATCTGTTTAAATAAATTAGTTGGGTCTCTACATGCATAACAACCC 360
Db 301 CAGCCTGTTTCTATCTGTTTAAATAAATTAGTTGGGTCTCTACATGCATAACAACCC 360
QY 361 TGCCTCAATCTGCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACCAAC 420
Db 361 TGCCTCAATCTGCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACCAAC 420
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Db 361 TGCCTCAATCTGCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACCAAC 420
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Db 421 TTTATTTTCTATGTTGTTTTTGCACATATGAGTGTGTTTGAATAAATAAGTACCCATGTC 480
QY 481 TTTA 484
Db 481 TTTA 484

RESULT 3
US-09-328-475C-334/c
; Sequence 334, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Cartoll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 334
; LENGTH: 2051
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2051)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-334
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Query Match 97.5%; Score 472; DB 4; Length 2051;
Best Local Similarity 99.6%; Pred. No. 1.7e-117;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 60
Db 854 TTTTAAATAAGCATTTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 795
QY 61 AATTTAAATCTTCAACTTGCAATTTGCAAGGATTACACATTTCACTCTGTATATATG 120
Db 794 AATTTAAATCTTCAACTTGCAATTTGCAAGGATTACACATTTCACTCTGTATATATG 735
QY 121 TGTGTC--AAAAAATAAAGTGTCTTTGTTTAAATTAATTTACTTGGTTGTAATCCATCT 178
Db 734 TGTGCAAAAAAATAAAGTGTCTTTGTTTAAATTAATTTACTTGGTTGTAATCCATCT 675
QY 179 GCTTTTCCCATTTGGAACCTAGTCATTAAACCCATCTCTGAACCTGTAGAAAAACATCTGA 238
Db 674 GCTTTTCCCATTTGGAACCTAGTCATTAAACCCATCTCTGAACCTGTAGAAAAACATCTGA 615
QY 239 AGAGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTCAACCCA 298
Db 614 AGAGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTCAACCCA 555
QY 299 GACAGCCTGTTTCTATCTGTTTAAATAAATTAGTTGGGTCTCTACATGCATAACAAC 358
Db 554 GACAGCCTGTTTCTATCTGTTTAAATAAATTAGTTGGGTCTCTACATGCATAACAAC 495
QY 359 CTTGCTCCATCTGCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACCA 418
Db 494 CTTGCTCCATCTGCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACCA 435
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Qy	419	ACTTTATTTTCTATG	TGTTTTTGGCAACATATGAGTGT	TTTTGAAAAATAAGTACCCATG	478
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Qy	479	TCCTTA	484		
Db	374	TCCTTA	369		

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RESULT 4
US-09-439-313-335
; Sequence 335, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 2984
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-335

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Query Match	97.5%	Score	472	DB	4	Length	2984		
Best Local Similarity	99.6%	Pred. No.	1.9e-117						
Matches	484	Conservative	0	Mismatches	0	Indels	2	Gaps	1

Qy	1	TTTTAAATAAGCATTTAGTGCCTCAGTCCTCTACTGAGTACTCTTTCTCTCCCTCCTCTG	60
Db	2473	TTTTAAATAAGCATTTAGTGCCTCAGTCCTCTACTGAGTACTCTTTCTCTCCCTCCTCTG	2532
Qy	61	AAATTAATCTTTCACATTCGCAATTTGCAAGGATTTACACATTTTCACTGTGATGTATATTG	120
Db	2533	AAATTAATCTTTCACATTCGCAATTTGCAAGGATTTACACATTTTCACTGTGATGTATATTG	2592
Qy	121	TGTTGC - -AAAAAAAAAAGTCTCTTTGTTTAAAAATTACTTGGTTTGTGAATCCATCTT	178
Db	2593	TGTTGCAAAAAAAAAAAGTCTCTTTGTTTAAAAATTACTTGGTTTGTGAATCCATCTT	2652
Qy	179	GCATTTTCCCATTTGGAAGTGTAGTCTTAACCCATCTCTGAAGTGGTAGAAAAACATCTGA	238
Db	2653	GCATTTTCCCATTTGGAAGTGTAGTCTTAACCCATCTCTGAAGTGGTAGAAAAACATCTGA	2712
Qy	239	AGAGCTAGTCTATCAGCATCTGCAGGTGAATTTGGATGGTTCTCAGAACCATTTCAACCA	298
Db	2713	AGAGCTAGTCTATCAGCATCTGCAGGTGAATTTGGATGGTTCTCAGAACCATTTCAACCA	2772
Qy	299	GACAGCGCTGTTTCTATCCTCTTTTAAATAATTAAGTTGGGTTCTCTACATGCATAACAAAC	358
Db	2773	GACAGCGCTGTTTCTATCCTGTTTAAATAATTAAGTTGGGTTCTCTACATGCATAACAAAC	2832
Qy	359	CCTGCTCCAATCTGTACATATAAAGTCTGTGACTTTGAAGTTTAAAGTACGACACCCCAACAA	418
Db	2833	CCTGCTCCAATCTGTACATATAAAGTCTGTGACTTTGAAGTTTAAAGTACGACACCCCAACAA	2892
Qy	419	ACTTTATTTTCTATGTGTTTTTTTGGCAACATATGAGTGTGTTTTGAAATAAAGTACCCATG	478
Db	2893	ACTTTATTTTCTATGTGTTTTTTTGGCAACATATGAGTGTGTTTTGAAATAAAGTACCCATG	2952

RESULT 6
US-09-232-149A-335
; Sequence 335, Application US/09232149A

Patent No. 6465611
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer Lynn
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
 TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
 FILE REFERENCE: 210121.427C6
 CURRENT APPLICATION NUMBER: US/09/232.149A
 NUMBER OF SEQ ID NOS: 338
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 335
 LENGTH: 2984
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-322-149A-335

Query Match 97.5%; Score 472; DB 4; Length 2984;
 Best Local Similarity 99.6%; Pred. No. 1.9e-117;
 Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY	1	TTTTAAATAAGCATTAGTGGTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG	60
Db	2473	TTTTAAATAAGCATTAGTGGTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG	2532
QY	61	AATTTAATCTTTCAACTTGCATTTGCAAGGATTACACATTTCACTGATGATATG	120
Db	2533	AATTTAATCTTTCAACTTGCATTTGCAAGGATTACACATTTCACTGATGATATG	2592
QY	121	TGTTGC--AAAAAAGAGTCTTTGTTTAAATTAATTTGTTTGAATCCATCTTGA	178
Db	2593	TGTTGCAAAAAAAGAGTCTTTGTTTAAATTAATTTGTTTGAATCCATCTTGA	2652
QY	179	GCTTTTCCCATTTGCACTAGTCAATTAACCATCTCTGAACCTGGTAGAAAAATCTGA	238
Db	2653	GCTTTTCCCATTTGCACTAGTCAATTAACCATCTCTGAACCTGGTAGAAAAATCTGA	2712
QY	239	AGAGCTAGTCTATCAGCATCTGACAGGTGAATGGATGGTCTCAGAACATTTACCCCA	298
Db	2713	AGAGCTAGTCTATCAGCATCTGACAGGTGAATGGATGGTCTCAGAACATTTACCCCA	2772
QY	299	GACAGCGTTTCTATCTGTTTAAATAATTAATTAATTAATTAATTAATTAATTAAT	358
Db	2773	GACAGCGTTTCTATCTGTTTAAATAATTAATTAATTAATTAATTAATTAATTAAT	2832
QY	359	CCTGCTCAATCTGTCACATAAAGTCTGTCAGTTGAAGTTTGTGTTTGAATAAAGTAC	418
Db	2833	CCTGCTCAATCTGTCACATAAAGTCTGTCAGTTGAAGTTTGTGTTTGAATAAAGTAC	2892
QY	419	ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCATG	478
Db	2893	ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCATG	2952
QY	479	TCCTTA 484	
Db	2953	TCCTTA 2958	

RESULT 7
 US-09-328-475C-102
 Sequence 102, Application US/09328475C
 Patent No. 6476207
 GENERAL INFORMATION:
 APPLICANT: Zhang, Jimmy
 APPLICANT: Astel, Jon H.
 APPLICANT: Carroll III, Eddie
 APPLICANT: Endege, Wilson O.
 APPLICANT: Ford, Donna M.
 APPLICANT: Monahan, John E.
 APPLICANT: Schlegel, Robert
 APPLICANT: Steinmann, Kathleen E.
 TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
 FILE REFERENCE: 1532.002/200130.463
 CURRENT APPLICATION NUMBER: US/09/328,475C
 CURRENT FILING DATE: 1999-06-09
 NUMBER OF SEQ ID NOS: 341
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 102
 LENGTH: 1020
 TYPE: DNA
 ORGANISM: Homo Sapien
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)-(1020)
 OTHER INFORMATION: n = A,T,C or G
 US-09-328-475C-102

Query Match 88.1%; Score 426.2; DB 4; Length 1020;
 Best Local Similarity 95.7%; Pred. No. 2.6e-105;
 Matches 449; Conservative 0; Mismatches 18; Indels 2; Gaps 1;

QY	6	AAATAAGCATTAGTGTCTAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTGAATTT	65
Db	66	AATTCGCCCTTTTCGAGCGCGCGCGGCGAGGTACTCTTTCTCTCCCTCCTCTGAATTT	125
QY	66	AATTCCTTTCACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATGTTG	125
Db	126	AATTCCTTTCACTTGCATTTGCAAGGATTACACATTTCACTGTGATGATATGTTG	185
QY	126	CAAAAAAAGAGTGTCTTTGTTTAAATTAATTTGTTGTTGTTGTTGTTGTTGTTGTTT	185
Db	186	C--AAAAAAGAGTGTCTTTGTTTAAATTAATTTGTTGTTGTTGTTGTTGTTT	243
QY	186	CCCATTTGGAAGTGTGATTAACCATCTCTGAACCTGTGAGTGTGAGTGTGAGTGTG	245
Db	244	CCCATTTGGAAGTGTGATTAACCATCTCTGAACCTGTGAGTGTGAGTGTGAGTGTG	303
QY	246	GTCTATCAGCATCTGACAGTGAATTTGATGGTCTCAGAACATTTTACCCAGACGCC	305
Db	304	GTCTATCAGCATCTGACAGTGAATTTGATGGTCTCAGAACATTTTACCCAGACGCC	363
QY	306	TGTTCTATCCCTTTTAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTA	365
Db	364	TGTTCTATCCCTTTTAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTA	423
QY	366	CAATCTGCACATAAAGTCTGTGACTTGAAGTTTGTGAGTGTGAGTGTGAGTGTGAG	425
Db	424	CAATCTGCACATAAAGTCTGTGACTTGAAGTTTGTGAGTGTGAGTGTGAGTGTGAG	483
QY	426	TTTTCTATGTGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACC 474	
Db	484	TTTTCTATGTGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACC 532	

RESULT 8
 US-09-328-475C-103/C
 Sequence 103, Application US/09328475C
 Patent No. 6476207
 GENERAL INFORMATION:
 APPLICANT: Zhang, Jimmy
 APPLICANT: Astel, Jon H.
 APPLICANT: Carroll III, Eddie
 APPLICANT: Endege, Wilson O.
 APPLICANT: Ford, Donna M.
 APPLICANT: Monahan, John E.
 APPLICANT: Schlegel, Robert
 APPLICANT: Steinmann, Kathleen E.
 TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
 TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
 FILE REFERENCE: 1532.002/200130.463
 CURRENT APPLICATION NUMBER: US/09/328,475C
 CURRENT FILING DATE: 1999-06-09
 NUMBER OF SEQ ID NOS: 341
 SOFTWARE: FastSeq for Windows Version 3.0

```

; SEQ ID NO 103
; LENGTH: 102
; TYPE: DNA
; ORGANISM: HOMO
; FEATURE:
; NAME/KEY: m
; LOCATION: (1
; OTHER INFOR
US-09-328-475C-1

```

Query Match	88.18;	Score 426.2;	DB 4;	Length 1021;
Best Local Similarity	95.7%;	Pred. No. 2.6e-105;		
Matches 449;	Conservative 0;	Mismatches 18;	Indels 2;	Gaps 1;
Qy	6	AAATAAGCATTTAGTGTCTCAGTCCTACTGAGTACTCTTTCTCTCCCTCCTCTGAATTT	65	
Db	561	AATTGCGCCITTCGAGCGCGCCGCGGCGAGGTACTCTTTCTCTCCCTCCTCTGAATTT	502	
Qy	66	AATTCITTTCAACTTGC AATTTGCAAGGATTTACACATTTCACTGATGATATATTTGCTGTG	125	
Db	501	AATTCITTTCAACTTGC AATTTGCAAGGATTTACACATTTCACTGATGATATATTTGCTGTG	442	
Qy	126	CAAAAAAAGTGTCTTTGTTTAAAAATTAACCTTGTGTTGTGAATCCATCTTCTCTTTT	185	
Db	441	C-----AAGTGTCTTTGTTTAAAAATTAACCTTGTGTTGTGAATCCATCTTCTCTTTT	384	
Qy	186	CCCATTTGGAACCTAGTCAATTAACCATCTCTGAACTGGTGAAGAAACATCTGAAGAGCTA	245	
Db	383	CCCATTTGGAACCTAGTCAATTAACCATCTCTGAACTGGTGAAGAAACATCTGAAGAGCTA	324	
Qy	246	GTCTATCAGCATCTGACAGGTGAATTCGATGGTTCTCAGAACCAATTTACCCAGACAGCC	305	
Db	323	GTCTATCAGCATCTGACAGGTGAATTCGATGGTTCTCAGAACCAATTTACCCAGACAGCC	264	
Qy	306	TGTTTCTATCCTGTTTAAATAATAGTTTGGGTTCTCTACATGCAATAACAAACCGTGCCTC	365	
Db	263	TGTTTCTATCCTGTTTAAATAATAGTTTGGGTTCTCTACATGCAATAACAAACCGTGCCTC	204	
Qy	366	CAATCTCTCACATAAAGTCTGTGACATTGAAGTTTGTAGTCAGCACCCCCACCAACTTTAT	425	
Db	203	CAATCTCTCACATAAAGTCTGTGACATTGAAGTTTGTAGTCAGCACCCCCACCAACTTTAT	144	
Qy	426	TTTTTCTATGTTTTTTTTTGCAACATATAGTGTTTTTTGAAAAATAAGTACC	474	
Db	143	TTTTTCTATGTTTTTTTTTGCAACATATAGTGTTTTTTGAAAAATAAGTACC	95	

RESULT 9

US-09-328-475C-223/c
; Sequence 223, Application US/09328475C
; Patent No. 6476207

; GENERAL INFORMATION:

```

: APPLICANT: Zhang, Jimmy
: APPLICANT: Astel, Jon H.
: APPLICANT: Carroll III, Eddie
: APPLICANT: Endge, Wilson O.
: APPLICANT: Ford, Donna M.
: APPLICANT: Monahan, John E.
: APPLICANT: Schlegel, Robert
: APPLICANT: Steinmann, Kathleen E.
: TITLE OF INVENTION: GENES AND GENE EXPRESSION
: TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED
: FILE REFERENCE: 1532.002/200130.463
: CURRENT APPLICATION NUMBER: US/09/328,475C
: CURRENT FILING DATE: 1999-06-09
: NUMBER OF SEQ ID NOS: 341
: SOFTWARE: FastSeq for Windows Version 3.0

```

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; SEQ ID NO 223
; LENGTH: 822
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: miR-125b-3p

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; LOCATION: (1)...(822)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-328-475C-223

Query Match	85.9%	Score 415.6;	DB 4;	Length 822;
Best Local Similarity	98.4%;	Pred. No. 1.7e-102;		
Matches 431;	Conservative	0;	Mismatches 4;	Indels 3; Gaps 1;
OV	37	GTACTCTTTCTCTCCCTCTCTGAAATTTTAAATCTTTTCAACTTTCGAATTTTCGAAGGATTA	96	

Qy	37	GTACTCTTTCTCTCCCTCTCTGAAATTTAAATCTTTTCAACTTGCAAATTTGCAAGGATTA	96
Db	510	GTACTCTTTCTCTCCCTCTCTGAAATTTAAATCTTTTCAACTTGCAAATTTGCAAGGATTA	451
Qy	97	CACATTTCACTGTGATGTATATTGTGTGCAGAAAAAAGAGTCTTTGTTTAAATTT	156
Db	450	CACATTTCACTGTGATGTATATTGTGTGTC---AAAAAAGAGTCTTTGTTTAAATTT	394
Qy	157	ACTTGGTTTGTGAATCCATCTTGCTTTTCCCATTTGGAACCTAGTCAATTAACCCATCTCT	216
Db	393	ACTTGGTTTGTGAATCCATCTTGCTTTTCCCATTTGGAACCTAGTCAATTAACCCATCTCT	334
Qy	217	GAAGTGGTGAAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGCACAGGTGAATTTGGATG	276
Db	333	GAAGTGGTGAAGAAAAACATCTGAAGAGCTAGTCTATCGGCATCTGCACAGGTGAATTTGGATG	274
Qy	277	GTCTCTCAGAACCATTTTCAACCCAGACGCTGTTTCTATCTCTGTTTAAATAAATAGTTTGG	336
Db	273	GTCTCTCAGAACCATTTTCAACCCAGACGCTGTTTCTCATCTCTGTTTAAATAAATAGTTTGG	214
Qy	337	GTCTCTACATGATACAAACCCGTGCTCCAACCTGTGCACATAAAAGTCTGTGACTTGA	396
Db	213	GTCTCTACATGATACAAACCCGTGCTCCAACCTGTGCACATAAAAGTCTGTGACTTGA	154
Qy	397	GTTTGTAGTCAGCACCCCAACCACTTTATTTTCTATGTGTTTTCGACACATAGAGT	456
Db	153	GTTTGTAGTCAGCACCCCAACCACTTTATTTTCTATGTGTTTTCGACACATAGAGT	94
Qy	457	TTTTGAAAAATAAGTACC	474
Db	93	TTTTGAAAAATAAGTACC	76

RESULT 10

US-09-328-475C-222
; Sequence 222, Application US/09328475C
; Patent No. 6476207

: GENERAL INFORMATION:

```

> ORGANIZATION:
> APPLICANT: Zhang, Jimmy
> APPLICANT: Astel, Jon H.
> APPLICANT: Carroll III, Eddie
> APPLICANT: Endege, Wilson O.
> APPLICANT: Ford, Donna M.
> APPLICANT: Monahan, John E.
> APPLICANT: Schlegel, Robert
> APPLICANT: Steinmann, Kathleen E.
> TITLE OF INVENTION: GENE AND GENE EXPRESSION PRODUCTS THAT
> ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
> FILE REFERENCE: 1532_002/200130_463
> CURRENT APPLICATION NUMBER: US/09/328,475C
> CURRENT FILING DATE: 1999-06-09
> NUMBER OF SEQ ID NOS: 341
> SOFTWARE: FastSeq for Windows Version 3.0
> SEQ ID NO 222
> LENGTH: 497
> TYPE: DNA
> ORGANISM: Homo Sapien
> US-09-328-475C-222

```

Query Match

Query Match	79.13;	Score 382.8;	DB 4;	Length 497;
Best Local Similarity	98.8%;	Pred. No. 9e-94;		
Matches 397;	Conservative	0;	Mismatches 2;	Indels 3; Gaps 1;
Qy	37	GTACTCTTTCTCTCCCTCCTCTGAAATTTAATTTCTTTCAACTTTCGAATTTGCAAGGATTA	96	

Db 99 GTACTCTTCTCCCTCCTCTGAATTTAAATTTCTTCAACTTGCAATTTGCAAGGATTA 158
QY 97 CACATTTCACTGTGATATATTTGTTGCAAAAAAAGTCTCTTTGTTAAATTT 156
Db 159 CACATTTCACTGTGATATATTTGTTGCAAAAAAAGTCTCTTTGTTAAATTT 215
QY 157 ACTTGTGTTGTAATCCATCTGCTTTTCCCATTTGGAATAGTCAATACCCATCTCT 216
Db 216 ACTTGTGTTGTAATCCATCTGCTTTTCCCATTTGGAATAGTCAATACCCATCTCT 275
QY 217 GAACTGGTGAAGAAACATCTGAAGAGCTAGTCTATCAGCATCTCAGAGGTGAATGGATG 276
Db 276 GAACTGGTGAAGAAACATCTGAAGAGCTAGTCTATCAGCATCTCAGAGGTGAATGGATG 335
QY 277 GTTCTCAGAACATTTCCACCAGAGAGCTGTTTCTATCTCTGTTTAAATAATAGTTGG 336
Db 336 GTTCTCAGAACATTTCCACCAGAGAGCTGTTTCTATCTCTGTTTAAATAATAGTTGG 395
QY 337 GTTCTCAGAACATTTCCACCAGAGAGCTGTTTCTATCTCTGTTTAAATAATAGTTGG 396
Db 396 GTTCTCAGAACATTTCCACCAGAGAGCTGTTTCTATCTCTGTTTAAATAATAGTTGG 455
QY 397 GTTCTCAGAACATTTCCACCAGAGAGCTGTTTCTATCTCTGTTTAAATAATAGTTGG 438
Db 456 GTTCTCAGAACATTTCCACCAGAGAGCTGTTTCTATCTCTGTTTAAATAATAGTTGG 497

RESULT 11
US-09-020-956-115
; Sequence 115, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, David C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
US-09-020-956-115

Query Match 75.4%; Score 365; DB 3; Length 366;
Best Local Similarity 100.0%; Pred. No. 4.9e-89;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 CTCTTCTCTCCCTCCTCTGAATTTAAATTTCTTCAACTTGCAATTTGCAAGGATTA 99
Db 2 CTCTTCTCTCCCTCCTCTGAATTTAAATTTCTTCAACTTGCAATTTGCAAGGATTA 61
QY 100 ATTCTACTGTGATGATATATTTGTTGCAAAAAAAGTCTCTTTGTTTAAATTTACT 159
Db 62 ATTCTACTGTGATGATATATTTGTTGCAAAAAAAGTCTCTTTGTTTAAATTTACT 121
QY 160 TGGTTTGTCAATCCATCTGCTTTTCCCATTTGGAATAGTCAATACCCATCTCTGAA 219
Db 122 TGGTTTGTCAATCCATCTGCTTTTCCCATTTGGAATAGTCAATACCCATCTCTGAA 181
QY 220 CTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTCAGAGGTGAATGGATGTT 279
Db 182 CTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTCAGAGGTGAATGGATGTT 241
QY 280 CTCAGAACCATTTCCACCAGAGAGCTGTTTCTATCTCTGTTTAAATAATAGTTGGGTT 339
Db 242 CTCAGAACCATTTCCACCAGAGAGCTGTTTCTATCTCTGTTTAAATAATAGTTGGGTT 301
QY 340 CTCTACATGCATAACAAACCTGCTCCAAATCTGTACATATAAGTCTGTGACTTGAAGTT 399
Db 302 CTCTACATGCATAACAAACCTGCTCCAAATCTGTACATATAAGTCTGTGACTTGAAGTT 361
QY 400 TAGTC 404
Db 362 TAGTC 366

RESULT 12
US-09-030-607-115
; Sequence 115, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
US-09-030-607-115

Qy	160	TGTTTTGGAATCCATCTTGTCTTTTCCCCATTGGAAC	TAGTCATTAACCCATCTCTGAA	219
Db	122	TGTTTTGTGAATCCATCTTGTCTTTTCCCCATTGGAAC	TAGTCATTAACCCATCTCTGAA	181
Qy	220	CTGTGAGAAAAACATCTGAAGAGCTAGTGTCTATCAGCATCTGACAGGTGAAT	TGGATGGGTT	279
Db	182	CTGTGAGAAAAACATCTGAAGAGCTAGTGTCTATCAGCATCTGACAGGTGAAT	TGGATGGGTT	241
Qy	280	CTCAGAACCATTTACCCAGACAGCGTGTCTCTATCCGTGTATATAAT	TAGTTTCGGTT	339
Db	242	CTCAGAACCATTTACCCAGACAGCGTGTCTCTATCCGTGTATATAAT	TAGTTTCGGTT	301
Qy	340	CTCTACATGCATAAACAACCGTGTCCAACTGTGCACATAAAAGTC	CTGTGACTTGAAGTT	399
Db	302	CTCTACATGCATAAACAACCGTGTCCAACTGTGCACATAAAAGTC	CTGTGACTTGAAGTT	361
Qy	400	TAGTC	404	
Db	362	TAGTC	366	

RESULT 14
US-09-352-616A-115
; Sequence 115, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocke, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13

```

; TITLE OF INVENTION: COMPOUNDS FOR TUMOROTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352.616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-115

Query Match 75.4%; Score 365; DB 4; Length 366;
Best Local Similarity 100.0%; Pred. No. 4.9e-89;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

[illegible]

QY 400 TAGTC 404
|||||
Db 362 TAGTC 366

RESULT 15

US-09-232-149A-115
: Sequence 115, Application US/09232149A
: Patent No. 6465611
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer Lynn
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
: FILE OF INVENTION: CANCER AND METHODS FOR THEIR USE
: FILE REFERENCE: 210121.427C6
: CURRENT APPLICATION NUMBER: US/09/232,149A
: NUMBER OF SEQ ID NOS: 338
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 115
: LENGTH: 366
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-232-149A-115

Query Match 75.4%; Score 365; DB 4; Length 366;
Best Local Similarity 100.0%; Pred. No. 4.9e-89;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 40 CTCCTTCTCCCTCCTCTGAAATTAATCTTCAACTTGCAATTTGCAAGGATTACAC 99
Db |||||||
2 CTCCTTCTCCCTCCTCTGAAATTAATCTTCAACTTGCAATTTGCAAGGATTACAC 61
QY 100 ATTCACTGTGATGATATGTTGTCGCAAAAAAAGTGTCTTTTAAAAATTACT 159
Db |||||||
62 ATTCACTGTGATGATATGTTGTCGCAAAAAAAGTGTCTTTTAAAAATTACT 121
QY 160 TGGTTTGTGAATCCATCTTGTCTTTTCCCATTTGGAACCTAGTCATTACCCATCTCTGAA 219
Db |||||||
122 TGGTTTGTGAATCCATCTTGTCTTTTCCCATTTGGAACCTAGTCATTACCCATCTCTGAA 181
QY 220 CTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTGGATGTT 279
Db |||||||
182 CTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGGTGAATTGGATGTT 241
QY 280 CTCAGAACCATTTACCCAGACAGCCTGTTTCTATCCTGTTTAAATAATTAGTTGGTT 339
Db |||||||
242 CTCAGAACCATTTACCCAGACAGCCTGTTTCTATCCTGTTTAAATAATTAGTTGGTT 301
QY 340 CTCTACATGCATAACAAACCCCTGCTCCAACTGTGTCACATAAAAGTCTGTGACTTGAAGTT 399
Db |||||||
302 CTCTACATGCATAACAAACCCCTGCTCCAACTGTGTCACATAAAAGTCTGTGACTTGAAGTT 361
QY 400 TAGTC 404
Db 362 TAGTC 366

Search completed: September 13, 2003, 03:05:40
Job time : 57 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 01:57:16 ; Search time 195 Seconds
(without alignments)
6025.816 Million cell updates/sec

Title: US-09-352-616A-434

Perfect score: 484

Sequence: 1 tttaaataagcatttagt.....ataaagtaccattgtttta 484

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1632420 seqs, 1213878141 residues

Total number of hits satisfying chosen parameters: 3264840

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	484	100.0	484	9	US-09-759-143-434
2	484	100.0	484	9	US-09-780-669-434
3	484	100.0	484	9	US-09-822-827-434
4	484	100.0	484	10	US-09-895-793-434
5	484	100.0	484	9	US-09-895-814-434
6	484	100.0	484	12	US-10-144-678A-434
7	484	100.0	484	13	US-10-012-896-434
8	484	100.0	484	14	US-10-010-940-434
9	473	97.7	755	10	US-09-925-300-258
10	472	97.5	2051	13	US-10-202-193-334
11	472	97.5	2984	9	US-09-759-143-335
12	472	97.5	2984	9	US-09-780-669-335
13	472	97.5	2984	9	US-09-822-827-335
14	472	97.5	2984	10	US-09-232-880-335
15	472	97.5	2984	10	US-09-895-793-335
16	472	97.5	2984	10	US-09-895-814-335

17	472	97.5	2984	12	US-10-144-678A-335	Sequence 335, App	
18	472	97.5	2984	13	US-10-012-896-335	Sequence 335, App	
19	472	97.5	2984	14	US-10-010-940-335	Sequence 335, App	
20	455.4	94.1	3266	14	US-10-205-823-282	Sequence 282, App	
21	426.2	88.1	1020	13	US-10-202-193-102	Sequence 102, App	
22	426.2	88.1	1021	13	US-10-202-193-103	Sequence 103, App	
23	415.6	85.9	822	13	US-10-202-193-223	Sequence 223, App	
C	24	382.8	79.1	497	13	US-10-202-193-222	Sequence 222, App
25	365	75.4	366	9	US-09-759-143-115	Sequence 115, App	
26	365	75.4	366	9	US-09-780-669-115	Sequence 115, App	
27	365	75.4	366	9	US-09-030-606-115	Sequence 115, App	
28	365	75.4	366	9	US-09-822-827-115	Sequence 115, App	
29	365	75.4	366	9	US-09-115-453-115	Sequence 115, App	
30	365	75.4	366	10	US-09-232-880-115	Sequence 115, App	
31	365	75.4	366	10	US-09-895-793-115	Sequence 115, App	
32	365	75.4	366	10	US-09-895-814-115	Sequence 115, App	
33	365	75.4	366	12	US-10-144-678A-115	Sequence 115, App	
34	365	75.4	366	13	US-10-012-896-115	Sequence 115, App	
35	365	75.4	366	14	US-10-010-940-115	Sequence 115, App	
C	36	360	74.4	374	10	US-09-969-708-40	Sequence 40, App
37	332	68.6	335	9	US-09-759-143-141	Sequence 141, App	
38	332	68.6	335	9	US-09-780-669-141	Sequence 141, App	
39	332	68.6	335	9	US-09-030-606-141	Sequence 141, App	
40	332	68.6	335	9	US-09-822-827-141	Sequence 141, App	
C	41	332	68.6	335	9	US-09-115-453-141	Sequence 141, App
42	332	68.6	335	10	US-09-232-880-141	Sequence 141, App	
43	332	68.6	335	10	US-09-895-793-141	Sequence 141, App	
44	332	68.6	335	10	US-09-895-814-141	Sequence 141, App	
C	45	332	68.6	335	12	US-10-144-678A-141	Sequence 141, App

ALIGNMENTS

RESULT 1

US-09-759-143-434
; Sequence 434, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09759.143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 434
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-759-143-434

Query Match 100.0%; Score 484; DB 9; Length 484;
Best local Similarity 100.0%; Pred. No. 7.7e-119;
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-434

Query Match      100.0%; Score 484; DB 10; Length 484;
Best Local Similarity 100.0%; Pred. No. 7,7e-119;
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTAAATAAGCATTTAGTGTCTAGTCCCTACTGAGTACACTCTTCTCTCCCTCCCTCTG 60
Db 1 TTTTAAATAAGCATTTAGTGTCTAGTCCCTACTGAGTACACTCTTCTCTCCCTCCCTCTG 60

QY 61 AATTTAAATCTTCAACTTGGCAATTTGCAAGGATTACACATTTCACTGTGATGATATTG 120
Db 61 AATTTAAATCTTCAACTTGGCAATTTGCAAGGATTACACATTTCACTGTGATGATATTG 120

QY 121 TGGTGCACAAAAAAGTCTCTTGTGTTTAAAAATTAAGTGGTTGTTGAATCAATCTGTC 180
Db 121 TGGTGCACAAAAAAGTCTCTTGTGTTTAAAAATTAAGTGGTTGTTGAATCAATCTGTC 180

QY 181 TTTTTCGCCATTTGAACTAGTCAATTAACCCATCTCTGAATGTTAGTAAAAACATCTGAAG 240
Db 181 TTTTTCGCCATTTGAACTAGTCAATTAACCCATCTCTGAATGTTAGTAAAAACATCTGAAG 240

QY 241 AGCTAGTCTATCAGCATCTGACAGGTGCAATGGATGTTCTCAGAACATTTTCAACCAGA 300
Db 241 AGCTAGTCTATCAGCATCTGACAGGTGCAATGGATGTTCTCAGAACATTTTCAACCAGA 300

QY 301 CAGCCTGTTTCTATCCGTTTAAATAATTAAGTTGGGTTCTCTACATGCATAACAACCC 360
Db 301 CAGCCTGTTTCTATCCGTTTAAATAATTAAGTTGGGTTCTCTACATGCATAACAACCC 360

QY 361 TGCTCCAATCTGCACATAAAAGTCTGTGACTTTGAAGTTTAGTCAGACCCCCACCAAC 420
Db 361 TGCTCCAATCTGCACATAAAAGTCTGTGACTTTGAAGTTTAGTCAGACCCCCACCAAC 420

QY 421 TTTATTTTCTATGTGTTTTTTCGACATATGAGTGTGTTGAAAAATAAGTACCCATGTC 480
Db 421 TTTATTTTCTATGTGTTTTTTCGACATATGAGTGTGTTGAAAAATAAGTACCCATGTC 480

QY 481 TTTA 484
Db 481 TTTA 484

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RESULT 6
US-10-144-678A-434
; Sequence 434, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.

```

; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 434
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-678A-434

Query Match      100.0%; Score 484; DB 12; Length 484;
Best Local Similarity 100.0%; Pred. No. 7.7e-119;
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTTAAATAAGCATTTAGTGTCTAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 60
DB      1 TTTTAAATAAGCATTTAGTGTCTAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 60

QY      61 AATTTAAATCTTTCAACTTGGCAATTTGCAAGGATTACACATTTACATGTCGATGATATTG 120
DB      61 AATTTAAATCTTTCAACTTGCATTTGCAAGGATTACACATTTACATGTCGATGATATTG 120

QY      121 TGTTCACAAAAAATAAGTGTCTTTGTTTAAAAATTACTTGGTTGTGAAATCCATCTTGC 180
DB      121 TGTTCACAAAAAATAAGTGTCTTTGTTTAAAAATTACTTGGTTGTGAAATCCATCTTGC 180

QY      181 TTTTTCGCCCATTTGGAACCTAGTGCATTAAACCCATCTCTGAACGTGTAGAAAAACATCTGAAG 240
DB      181 TTTTTCGCCCATTTGGAACCTAGTGCATTAAACCCATCTCTGAACGTGTAGAAAAACATCTGAAG 240

QY      241 AGCTAGTCTATCAGCATCTGACAGGTGAATGATGTTCTTCAGAACCATTTTCAACCAGA 300
DB      241 AGCTAGTCTATCAGCATCTGACAGGTGAATGATGTTCTTCAGAACCATTTTCAACCAGA 300

QY      301 CAGCCTGTTTCTATCCCTGTTTAAATAAATTAGTTTGGTTCCTACATGCATATAACAACCC 360
DB      301 CAGCCTGTTTCTATCCCTGTTTAAATAAATTAGTTTGGTTCCTACATGCATATAACAACCC 360

QY      361 TGTCTCAATCTGTCACATAAAAGTCTGTGACTTTGAGTTTGTAGTCAGCACCCCCCACCACAAAC 420
DB      361 TGTCTCAATCTGTCACATAAAAGTCTGTGACTTTGAGTTTGTAGTCAGCACCCCCCACCACAAAC 420

QY      421 TTTATTTTCTATGTCGTTTTTTCGACATATGAGTGTTTTGAAATAAAGTACCCCATGTC 480
DB      421 TTTATTTTCTATGTCGTTTTTTCGACATATGAGTGTTTTGAAATAAAGTACCCCATGTC 480

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RESULT 7
US - 010-012-896-434
; Sequence 434, Application US/10012896
; Publication No. US20020193251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Ditcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jilang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Ketter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.

```

; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Magdelaine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 434
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-434

Query Match 100.0%; Score 484; DB 13; Length 484;
Best Local Similarity 100.0%; Pred. No. 7.7e-119;
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTTAAATAGCAATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 60
Db 1 TTTTAAATAGCAATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 60
Qy 61 AATTAAATCTTCAACTTGCATTTTCAAGGATTACACATTTCCACGTGATGATATG 120
Db 61 AATTAAATCTTCAACTTGCATTTTCAAGGATTACACATTTCCACGTGATGATATG 120
Qy 121 TGTGCAAAAAAAGAGTCTCTTTGTTTAAATTTACTTGGTTTGAATCCATCTTGC 180
Db 121 TGTGCAAAAAAAGAGTCTCTTTGTTTAAATTTACTTGGTTTGAATCCATCTTGC 180
Qy 181 TTTTCCCATTTGGAATCTGATTAACCCATCTCTGAACCTGTTAGTGAATCCATCTGAAG 240
Db 181 TTTTCCCATTTGGAATCTGATTAACCCATCTCTGAACCTGTTAGTGAATCCATCTGAAG 240
Qy 241 AGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTTCAACCCAGA 300
Db 241 AGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTTCAACCCAGA 300
Qy 301 CAGCCTGTTCTATCTCTGTTTAAATTTAGTTTGGGTTCTCTACATGCATAACAAACCC 360
Db 301 CAGCCTGTTCTATCTCTGTTTAAATTTAGTTTGGGTTCTCTACATGCATAACAAACCC 360
Qy 361 TGCTCCCAATCTGTCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACAAAC 420
Db 361 TGCTCCCAATCTGTCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACAAAC 420
Qy 421 TTTATTTTCTATCTGTTTGTGCAACATATGAGTGTGTTGAAATTAAGTACCACATGTC 480
Db 421 TTTATTTTCTATCTGTTTGTGCAACATATGAGTGTGTTGAAATTAAGTACCACATGTC 480
Qy 481 TTTA 484
Db 481 TTTA 484

RESULT 8
US-10-010-940-434
; Sequence 434, Application US/10010940
; Publication No. US20030088062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925.300

; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010.940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 434
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-940-434

Query Match 100.0%; Score 484; DB 14; Length 484;
Best Local Similarity 100.0%; Pred. No. 7.7e-119;
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTTAAATAGCAATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 60
Db 1 TTTTAAATAGCAATTTAGTGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCCTCTG 60
Qy 61 AATTAAATCTTCAACTTGCATTTTCAAGGATTACACATTTCCACGTGATGATATG 120
Db 61 AATTAAATCTTCAACTTGCATTTTCAAGGATTACACATTTCCACGTGATGATATG 120
Qy 121 TGTGCAAAAAAAGAGTCTCTTTGTTTAAATTTACTTGGTTTGAATCCATCTTGC 180
Db 121 TGTGCAAAAAAAGAGTCTCTTTGTTTAAATTTACTTGGTTTGAATCCATCTTGC 180
Qy 181 TTTTCCCATTTGGAATCTGATTAACCCATCTCTGAACCTGTTAGTGAATCCATCTGAAG 240
Db 181 TTTTCCCATTTGGAATCTGATTAACCCATCTCTGAACCTGTTAGTGAATCCATCTGAAG 240
Qy 241 AGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTTCAACCCAGA 300
Db 241 AGCTAGTCTATCAGCATCTGACAGTGAATTTGGATGTTCTCAGAACCATTTTCAACCCAGA 300
Qy 301 CAGCCTGTTCTATCTCTGTTTAAATTTAGTTTGGGTTCTCTACATGCATAACAAACCC 360
Db 301 CAGCCTGTTCTATCTCTGTTTAAATTTAGTTTGGGTTCTCTACATGCATAACAAACCC 360
Qy 361 TGCTCCCAATCTGTCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACAAAC 420
Db 361 TGCTCCCAATCTGTCACATAAAAGTCTGTGACTTGAAGTTTGTAGTCAGCACCCCAACAAAC 420
Qy 421 TTTATTTTCTATCTGTTTGTGCAACATATGAGTGTGTTGAAATTAAGTACCACATGTC 480
Db 421 TTTATTTTCTATCTGTTTGTGCAACATATGAGTGTGTTGAAATTAAGTACCACATGTC 480
Qy 481 TTTA 484
Db 481 TTTA 484

RESULT 9
US-09-925-300-258
; Sequence 258, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Ruben
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925.300

; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1990
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 258
; LENGTH: 755
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (755)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-258

Query Match 97.7%; Score 473; DB 10; Length 755;
Best Local Similarity 99.8%; Pred. No. 8e-116;
Matches 484; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 1 TTTTAAATAAGCATTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 60
Db 242 TTTTAAATAAGCATTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 301
QY 61 AATTTAAATCTTCAACTTGAATTTGCAAGGATTACAAATTTCACTGTGATATATTG 120
Db 302 AATTTAAATCTTCAACTTGAATTTGCAAGGATTACAAATTTCACTGTGATATATTG 120
QY 121 TGTGTC-AAAAAAGTCTCTTTGTTTAAATTTACTTGTGTTGAATCCATCTTG 179
Db 362 TGTGTC-AAAAAAGTCTCTTTGTTTAAATTTACTTGTGTTGAATCCATCTTG 421
QY 180 CTTTTCCTCCATTTGGAATAGTCTATTAACCCATCTCTGAACTGGTAGAAAAACATCTGAA 239
Db 422 CTTTTCCTCCATTTGGAATAGTCTATTAACCCATCTCTGAACTGGTAGAAAAACATCTGAA 481
QY 240 GAGTAGTCTATCAGCATCTGACAGGTGAATGGATGTTCTCAGAACCATTTACCCAG 299
Db 482 GAGTAGTCTATCAGCATCTGACAGGTGAATGGATGTTCTCAGAACCATTTACCCAG 541
QY 300 ACAGCCTGTTCTATCTCTGTTTAAATTAATAGTTGGGTTCTCTACATGCAACAAACC 359
Db 542 ACAGCCTGTTCTATCTCTGTTTAAATTAATAGTTGGGTTCTCTACATGCAACAAACC 601
QY 360 CTGCTCAATCTGTCACATAAAGTCTGTGACTTTGAAGTTTAGTCAGCACCCCCACCAAA 419
Db 602 CTGCTCAATCTGTCACATAAAGTCTGTGACTTTGAAGTTTAGTCAGCACCCCCACCAAA 661
QY 420 CTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCCATGT 479
Db 662 CTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCCATGT 721
QY 480 CTTTA 484
Db 722 CTTTA 726
```

RESULT 10

US-10-202-193-334/c
; Sequence 334, Application US/10202193
; Publication NO. US20020192699A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER

; FILE REFERENCE: PP-01532.103/200130.463DI
; CURRENT APPLICATION NUMBER: US/10/202,193
; CURRENT FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 334
; LENGTH: 2051
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2051)
; OTHER INFORMATION: n = A,T,C or G
US-10-202-193-334

Query Match 97.5%; Score 472; DB 13; Length 2051;
Best Local Similarity 99.6%; Pred. No. 2.4e-115;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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QY 1 TTTTAAATAAGCATTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 60
Db 854 TTTTAAATAAGCATTAGTCTCAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCTG 795
QY 61 AATTTAAATCTTCAACTTGAATTTGCAAGGATTACAAATTTCACTGTGATATATTG 120
Db 794 AATTTAAATCTTCAACTTGAATTTGCAAGGATTACAAATTTCACTGTGATATATTG 120
QY 121 TGTGTC-AAAAAAGTCTCTTTGTTTAAATTTACTTGTGTTGAATCCATCTT 178
Db 734 TGTGTC-AAAAAAGTCTCTTTGTTTAAATTTACTTGTGTTGAATCCATCTT 675
QY 179 GCTTTTCCCATTTGGAATAGTCTATTAACCCATCTCTGAACTGGTAGAAAAACATCTGA 238
Db 674 GCTTTTCCCATTTGGAATAGTCTATTAACCCATCTCTGAACTGGTAGAAAAACATCTGA 615
QY 239 AGAGCTAGTCTATCAGCATCTGACAGGTGAATGGATGTTCTCAGAACCATTTACCCA 298
Db 614 AGAGCTAGTCTATCAGCATCTGACAGGTGAATGGATGTTCTCAGAACCATTTACCCA 555
QY 299 GACAGCCTGTTCTATCTCTGTTTAAATTAATAGTTGGGTTCTCTACATGCAACAAAC 358
Db 554 GACAGCCTGTTCTATCTCTGTTTAAATTAATAGTTGGGTTCTCTACATGCAACAAAC 495
QY 359 CTGCTCCAATCTGTCACATAAAGTCTGTGACTTTGAAGTTTAGTCAGCACCCCCACCAA 418
Db 494 CTGCTCCAATCTGTCACATAAAGTCTGTGACTTTGAAGTTTAGTCAGCACCCCCACCAA 435
QY 419 ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCCATG 478
Db 434 ACTTTATTTTCTATGTTTGTGCAACATATGAGTGTGTTTGAATAAAGTACCCATG 375
QY 479 TCTTTA 484
Db 374 TCTTTA 369
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RESULT 11

US-09-759-143-335
; Sequence 335, Application US/09759143
; Patent No. US200202248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.

:	APPLICANT:	Stolk, John A.
:	APPLICANT:	Day, Craig H.
:	APPLICANT:	Vedvick, Thomas S.
:	APPLICANT:	Carter, Darrick
:	APPLICANT:	Li, Samuel
:	APPLICANT:	Wang, Aijun
:	APPLICANT:	Skeiky, Yasir A.W.
:	APPLICANT:	Hepner, William
:	APPLICANT:	Hural, John
:	APPLICANT:	McNeill, Patricia D.
:	APPLICANT:	Houghton, Raymond L.
:	TITLE OF INVENTION:	COMPOSITIONS AND METHODS FOR THE THERAPY AND
:	TITLE OF INVENTION:	DIAGNOSIS OF PROSTATE CANCER
:	FILE REFERENCE:	210121.427C24
:	CURRENT APPLICATION NUMBER:	US/09/780,669
:	CURRENT FILING DATE:	2001-02-09
:	NUMBER OF SEQ ID NOS:	943
:	SOFTWARE:	FastSeq for Windows Version 3.0
:	SEQ ID NO 335	
:	LENGTH:	2984
:	TYPE:	DNA
:	ORGANISM:	Homo sapien
:	US-09-780-669-335	
Query Match 97.5%; Score 472; DB 9; Length 2984;		
Best Local Similarity 99.6%; Pred. No. 2.9e-115;		
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;		
Qy	1	TTTTAAATAAGCATTTAGTGCTTCAGTCCCTACTGAGTACTCTTCTCTCCCCTCCTCTG 60
Db	2473	TTTTAAATAAGCATTTAGTGCTTCAGTCCCTACTGAGTACTCTTCTCTCCCCTCCTCTG 2532
Qy	61	AATTTAATCTTCAACCTGCATTTGCCAAGGATTACACATTTACATGTGATGTATATTG 120
Db	2533	AATTTAATCTTCAACCTGCATTTGCCAAGGATTACACATTTACATGTGATGTATATTG 2592
Qy	121	TGTTGC--AAAAAAAAGTGTCTTTGGTTTAAAAATTAATTTGTTTGAATCCATCTT 178
Db	2593	TGTTGCAAAAAAAAAAGTGTCTTTGGTTTAAAAATTAATTTGTTTGAATCCATCTT 2652
Qy	179	GCTTTTCCCCNTGGAACTAGTCATTAACCCATCTCGAACCTGGTAGAAAAACATCTGA 238
Db	2653	GCTTTTCCCCATTTGGAACCTAGTCATTAACCCATCTCTGAACCTGGTAGAAAAACATCTGA 2712
Qy	239	AGAGCTAGTCTATCAGCATCTGCAGGTGAATTTGGATGGTTCTCAGAACCATTTTCACCCA 298
Db	2713	AGAGCTAGTCTATCAGCATCTGCAGGTGAATTTGGATGGTTCTCAGAACCATTTTCACCCA 2772
Qy	299	GACAGCCTGTTTCTATCCTCTTTAATAAATTAAGTTTGGGTTCTCTACATGCATAACAAC 358
Db	2773	GACAGCCTGTTTCTATCCTCTTTAATAAATTAAGTTTGGGTTCTCTACATGCATAACAAC 2832
Qy	359	CTTGCTCCAATCTGTCACATAAAGTCTGTGACTTGAAGTTTAGTCAGCACCCACCACCAA 418
Db	2833	CCTGCTCCAATCTGTCACATAAAGTCTGTGACTTGAAGTTTAGTCAGCACCCACCACCAA 2892
Qy	419	ACTTTATTTTCTATGTGTTTTTTTGGCAACATATGAGTGTTTTGAAATAAAGTACCACATG 478
Db	2893	ACTTTATTTTCTATGTGTTTTTTTGGCAACATATGAGTGTTTTGAAATAAAGTACCACATG 2952
Qy	479	TCTTTA 484
Db	2953	TCTTTA 2958
RESULT 13		
US-09-822-827-335		
:	Sequence 335,	Application US/09822827
:	Patent No. US20020081680A1	
:	GENERAL INFORMATION:	
:	APPLICANT:	Xu, Jiangchun
:	TITLE OF INVENTION:	COMPOSITIONS AND METHODS FOR THE THERAPY AND
:	TITLE OF INVENTION:	DIAGNOSIS OF PROSTATE CANCER

; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 2984
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-793-335

Query Match . 97.5%; Score 472; DB 10; Length 2984;
Best Local Similarity 99.6%; Pred. No. 2.9e-115;
Matches 484; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
Qy 1 TTTTAAATAAGCAATTAGTGCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCCCTCTG 60
Db TTTTAAATAAGCAATTAGTGCTCAGTCCCTACTGAGTACTCTTCTCTCCCTCCCTCTG 2532
Qy 61 AATTTAATCTTTCAACTTGCAGTTCGAATTTCAAGGATTACACATTTTCACATGATATATTG 120
Db AATTTAATCTTTCAACTTGCAGTTCGAATTTCAAGGATTACACATTTTCACATGATATATTG 2592
Qy 121 TGTTCG--AAAAAAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTT 178
Db TGTTCG--AAAAAAGTGTCTTTGTTTAAATTTACTTGGTTTGTGAATCCATCTT 2652
Qy 179 GCTTTTCCCATTTGGAAGTACTGATTAACCCATCTCTGAAGTGGTAGAAAAACATCTGA 238
Db GCTTTTCCCATTTGGAAGTACTGATTAACCCATCTCTGAAGTGGTAGAAAAACATCTGA 2712
Qy 239 AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTCTCAGAACCATTTTCACCCA 298
Db AGAGCTAGTCTATCAGCATCTGACAGGTGAATTTGGATGGTCTCAGAACCATTTTCACCCA 2772
Qy 299 GACAGCCTGTTCTATCTCTGTTTAAATTAATTTAGTTTGGGTTCTCTACATGCATAACAAAC 358
Db GACAGCCTGTTCTATCTCTGTTTAAATTAATTTAGTTTGGGTTCTCTACATGCATAACAAAC 2832
Qy 359 CCTGCTCAATCTGTACATAAAAGTCTGTGACTTTGAAGTTTACTGACACCCCCACCAA 418
Db CCTGCTCAATCTGTACATAAAAGTCTGTGACTTTGAAGTTTACTGACACCCCCACCAA 2892
Qy 419 ACTTTATTTTCTATGTGTTTTTGGCAACATATGAGTGTGTTGAAAATAAGTACCCATG 478
Db ACTTTATTTTCTATGTGTTTTTGGCAACATATGAGTGTGTTGAAAATAAGTACCCATG 2952
Qy 479 TCTTTA 484
Db TCTTTA 2958

Search completed: September 13, 2003, 03:09:03
Job time : 197 secs

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